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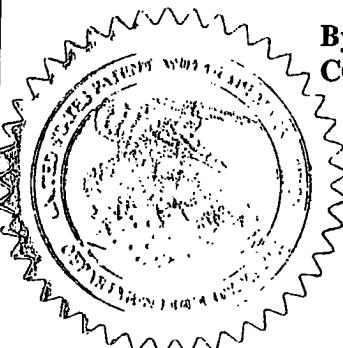
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE



In re the application of: Yocum, et al.

Attorney
Docket No. BGI-152-3

For: Methods and Organisms for Production of B6 Vitamers

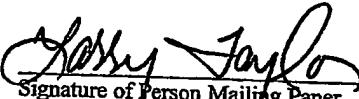
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CERTIFICATION UNDER 37 CFR 1.10

Date of Deposit: March 29, 2002Mailing Label Number: EL 833 314 145 US

I hereby certify that this Cover Sheet for Filing Provisional Application (37 C.F.R. §1.51(2)(i)) and the documents referred to as attached therein are being deposited with the United States Postal Service on the date indicated above in an envelope as "Express Mail Post Office to Addressee" service under 37 CFR 1.10 and addressed to the Commissioner for Patents, Box Provisional Patent Application, Washington, D.C. 20231.

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COVER SHEET FOR FILING PROVISIONAL PATENT APPLICATION

Dear Sir:

The accompanying application, entitled "Methods and Organisms for Production of B6 Vitamers," is a provisional patent application under 37 C.F.R. §1.51(c) and §1.53(c).

1. The name(s) and address(es) of the inventor(s) of this application is/are as follows:

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2. The following documents are enclosed:

- 28 page(s) of Specification
- 6 page(s) of Claims
- 1 page(s) of Abstract
- 12 page(s) of Sequence Listing
- 7 sheets of Informal Drawings; and
- Return postcard.

3. The fee for filing this provisional application, as set forth in 37 CFR 1.16(k), is \$160.00.

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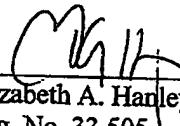
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5. Please address all future communications to: Customer Number: 000959 whose address is:

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METHODS AND ORGANISMS FOR PRODUCTION OF B6 VITAMERS

Background of the Invention

5 Vitamin B6, also known as pyridoxine or pyridoxol (PN), or one of a number of closely related compounds, is an essential dietary nutrient for most, if not all, animals, while many micro-organisms (bacteria, fungi, algae, etc.) and plants are capable of synthesizing their own vitamin B6 or compound(s) related to vitamin B6.

10 When an animal ingests PN or a related compound that has vitamin B6 activity, the compound is converted ultimately into pyridoxal phosphate (PLP) and/or pyridoxamine phosphate (PMP), which are the active forms of vitamin B6 in all living organisms. PLP acts as a cofactor for many important or essential enzymes in all living organisms, including transaminases, racemases, and decarboxylases. PLP and PMP are easily interconverted by ubiquitous transaminases.

15 Vitamin B6 is of commercial importance in vitamin pills, pharmaceutical applications, and as an animal feed additive that enhances growth or desirable growth characteristics in farm and domestic animals. The currently used commercial process for producing vitamin B6 is a synthetic chemical process. However, a fermentation process using a microorganism (see US Patent application No. 09/667,569, filed

20 September 21, 2000, hereby incorporated in its entirety by reference) or a biosynthetic process using a plant species can be more cost effective in the long run, and may be environmentally more attractive.

The biosynthetic pathway for PLP in *E. coli* has been elucidated (reviewed in Mittengruber, G., (2001) *J. Mol. Microbiol. Biotechnol.* 3(1): 1-20; Cane, D.E., et al. (2000) *J. Am. Chem. Soc.* 122: 4213-4214; Man, T-K, et al., (1996) *J. Bacteriol.* 178: 2445-2449). Enzymes encoded by the genes *epd*, *pdxB*, *pdxF*, and *pdxA* lead to synthesis of the precursor 1-hydroxy-3-amino acetone phosphate from erythrose-4-phosphate and glutamate. The enzyme encoded by *dxs* leads to the precursor 5'-deoxyxylulose phosphate from glycolytic intermediates. The enzyme encoded by *pdxJ* then catalyzes the chemical coupling of the two precursors to give pyridoxol phosphate (also called pyridoxine phosphate or PNP). PNP is then oxidized to the active form, PLP, by the enzyme encoded by *pdxH*. This biosynthetic pathway to PLP in *E. coli*, as well as closely related pathways, are referred to herein as the Type A Pathway. Partially characterized mutants of *E. coli* have been described that produce about three- to seven-fold more vitamin B₆-related compounds than the parent strain (Dempsey and Arcement (1971) *J. Bacteriol.* 107(2): 580-582). Partially characterized mutants of *B. subtilis* have been reported that produce 1 - 5 mg/l vitamin B₆, but it was not stated what level the

parent strain produced (Pflug, W., and Lingens, F., (1978) Hoppe-Seyler's Z. Physiol. Chem. 359: 559-570). Notably, these organisms were not recombinantly produced.

A second biosynthetic pathway for vitamin B6, referred to herein as the Type B pathway, may exist in some organisms other than *E. coli* (Mittengruber, G.,

5 (2001) *J. Mol. Microbiol. Biotechnol.* 3(1):1-20). In particular, some fungi (for example from the genera *Cercospora*, *Neurospora*, *Aspergillus* and *Saccharomyces*), some bacteria (for example *B. subtilis* and *Staphylococcus aureus*), and all plants for which data exists do not contain any genes that are highly homologous to *E. coli* *pdxA* and *pdxJ*. Instead, these organisms contain genes that are homologous to *Cercospora* genes 10 named *SOR* (or *SNZ*) and *SNO*. In *Saccharomyces*, these homologs are called *PDX1* and *PDX2*, respectively, and in *B. subtilis*, these homologs are named *yaaD* and *yaaE*, respectively. In *B. subtilis*, there have been no reports as to whether *yaaD* or *yaaE* are actually involved in PLP biosynthesis. Protein or DNA sequence homology alone is not sufficient to establish biological function. For example, *B. subtilis* contains a gene, 15 *yhaF*, that encodes a protein that is significantly homologous to *E. coli* *pdxF*. However, when *yhaF* is mutated, the resulting mutant *B. subtilis* strain is a serine auxotroph, but not a PL auxotroph (see Example 3, below). Thus, the identification of a gene or genes involved in PLP biosynthesis in any given organism can not be done using sequence homology alone.

20 Results from ¹³C and ¹⁵N labeling studies suggest that the precursors that provide the carbon and nitrogen atoms in PL and related compounds are different in *E. coli* and *Saccharomyces cerevisiae* (Gupta, R., et al. (2001) *J. Am Chem. Soc.* 123: 11353-11359; Tayuza, K., et al. (1995) *Biochim. Biophys. Acta* 1244: 113-116.) However, the identity of the precursors for PL and related compounds in *S. cerevisiae* is 25 not yet known. Since most micro-organisms for which the entire genome sequence is known (for example *E. coli*, *S. cerevisiae* and *B. subtilis*) have either *pdxA* and *pdxJ* homologs or *SOR* and *SNO* homologs, but not both, it appears that most organisms that are capable of synthesizing PLP have either the well characterized Type A Pathway (for example *E. coli*, *Salmonella typhimurium*, and many other genera), or a distinctly 30 different and incompletely characterized pathway, e.g., the Type B Pathway. Specifically, members of the genera *Cercospora*, *Neurospora*, *Aspergillus*, *Saccharomyces*, *Bacillus*, *Arabidopsis*, and many other genera, appear to have a Type B pathway, and are lacking genes involved in the Type A Pathway. The intermediate compounds in the Type B Pathway have not yet been elucidated, although the final 35 product must be PLP (as for the Type A Pathway) or PMP, since these are the active forms of vitamin B6 in all known organisms.

Summary of the Invention

The present invention is based, at least in part, on the discovery of key enzyme-encoding genes of the B6 vitamer biosynthetic pathways in *Bacillus subtilis*. In particular, the invention is based, at least in part, on the discovery that the *yaaD* and 5 *yaaE* genes of *B. subtilis* are required for B6 vitamer synthesis. Deletion of a portion of the *yaaD* and *yaaE* genes (which are adjacent in an operon, e.g., the *yaaDE* operon) leads to PL auxotrophy. Overexpression of the *yaaDE* operon or the deregulation of the expression of the *yaaD* or *yaaE* genes leads to significantly increased production of B6 vitamers in, e.g., *B. subtilis* strains. The *B. subtilis* *yaaDE* operon is required for 10 pyridoxal phosphate (PLP) biosynthesis, an active form of vitamin B6 in all living organisms. The present invention describes that the expression of the *B. subtilis* *yaaDE* operon is a rate limiting step for production of compounds related to vitamin B6 in a wild type strain.

Accordingly, the present invention features methods of producing B6 15 vitamers, including, but not limited to, pyridoxine (or pyridoxol (PN)), pyridoxal (PL), pyridoxamine (PM), or the 5' phosphorylated derivatives of any of the three aforementioned compounds (PNP, PLP, and PMP), using organisms in which the B6 vitamer pathway has been manipulated such that B6 vitamers are produced. Such methods include culturing a microorganism that overexpresses at least one B6 vitamer biosynthetic enzyme (e.g., at least one of the *yaaD* or *yaaE* gene products), under 20 conditions such that the B6 vitamer is produced. The production methods of the present invention further can include recovering the B6 vitamer.

The instant invention also features genetically modified organisms (i.e., 25 organisms that contain one or more modifications or mutations in the genome) that are capable of producing significantly more of a B6 vitamer than an unmodified parent organism. In particular, this invention features micro-organisms (including, for example, but not limited to, bacteria, yeasts, fungi, and algae) or macro-organisms such as plants that, when genetically modified, produce an increased amount, e.g., at least about 10-fold more of a B6 vitamer, than the unmodified parent organism. Specific 30 examples are given herein in which *Bacillus subtilis* and *Escherichia coli* strains have been genetically modified such that they produce significant amounts of a B6 vitamer. Accordingly, the present invention features organisms that have been genetically modified to increase the activity of one or more enzymes that catalyze(s) a step in the biosynthesis of a B6 vitamer, such that B6 vitamer production from said modified 35 organism is increased compared to B6 production in an unmodified parent organism.

Yet another aspect of the invention features recombinant microorganisms which overexpress at least one *Bacillus* (e.g., *B. subtilis*) B6 vitamer biosynthetic

enzyme (e.g., at least one of the *yaaD* or *yaaE* gene products) are described. In one embodiment, the recombinant microorganism is Gram positive (e.g., microorganisms belonging to the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*). In another embodiment, the recombinant microorganism is Gram negative. Particularly preferred is a *Bacillus* recombinant microorganism (e.g., *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus subtilis*, *Bacillus pumilus*, *Bacillus halodurans*, and the like).

Recombinant vectors that contain genes encoding *Bacillus* B6 vitamer biosynthetic enzymes, e.g., *yaaD* or *yaaE* genes, are also described.

10

Other features and advantages of the invention will be apparent from the following detailed description and claims.

Brief Description of the Drawings

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Figure 1 depicts the chemical structures of vitamin B6 and related compounds.

Figure 2 depicts the biosynthetic pathway for PLP in *E. coli*.

20

Figure 3 depicts the standard curves generated by *Saccharomyces unarum* strain ATCC 9080 after feeding serial dilutions of PN, PL, and PM (as described in Example 1).

Figure 4 is a schematic representation of the plasmid pDX1F.

Figure 5 is a schematic representation of the plasmid pDX11F.

Figure 6 is a schematic representation of the plasmid pDX14R.

Figure 7 is a schematic representation of the plasmid pDX17R.

25

Detailed Description of the Invention

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The present invention is based, at least in part, on the identification of *Bacillus* (e.g., *B. subtilis*) genes that encode essential enzymes of the B6 vitamer biosynthetic pathway. In particular, the present invention features methods based on manipulation of the B6 vitamer biosynthetic pathway in a microorganism such that certain desirable compounds are produced.

35

In particular, the invention is based, at least in part, on the discovery that the *yaaD* and *yaaE* genes of *B. subtilis* are required for B6 vitamer synthesis, including, but not limited to, pyridoxine (or pyridoxol (PN)), pyridoxal (PL), pyridoxamine (PM), or the 5' phosphorylated derivatives of any of the three aforementioned compounds (PNP, PLP, and PMP). The *yaaD* and *yaaE* genes are adjacent on an operon, e.g., the *yaaDE* operon. The *yaaD* and *yaaE* genes encode the YaaD and Yaa E proteins,

respectively. Overexpression of the *yaaDE* operon with a strong constitutive promoter or the deregulation of the expression of the *yaaD* or *yaaE* gene(s) leads to significantly increased production of B6 vitamers. These quantities are significantly higher relative to the associated parent strains than those reported in previous studies, which have

5 employed mutant *E. coli* strains (Dempsey and Arcement (1971) *J. Bacteriol.* 107 (2): 580-582), or mutant *B. subtilis* strains (Pflug, W., and Lingens, F., (1978) Hoppe-Seyler's *Z. Physiol. Chem.* 359: 559-570).

Accordingly, the present invention features organisms that have been genetically modified to increase the activity of one or more enzymes that catalyze a step 10 in the biosynthesis of a B6 vitamer, such that B6 vitamer production from the modified organism is increased compared to B6 production in an unmodified parent organism. In one embodiment, B6 vitamer production is at least ten-fold higher than from the unmodified parent organism. In another embodiment, the organism is genetically modified to overexpress one or more genes that encodes an enzyme that catalyzes a step 15 in the biosynthesis of a B6 vitamer, e.g., *yaaD* or *yaaE*. The organism may be, for example, *B. subtilis*.

The present invention also features methods of producing a B6 vitamer comprising culturing a microorganism that has been genetically modified to overexpress one or more genes that encodes an enzyme that catalyzes a step in the biosynthesis of a 20 B6 vitamer, such that B6 vitamer production from said modified organism is increased compared to B6 production in an unmodified parent organism, under conditions such that the B6 vitamer is produced. The B6 vitamer may then be subsequently recovered. Overproduction of the rate limiting enzyme for B6 vitamer production in any organism that is capable of producing B6 vitamers will lead to overproduction of B6 vitamers.

25 The terms "B6 vitamer" or "B6 vitamers," as used herein, shall refer to any compound or mixture of compounds that has any biological activity in any biological assay for vitamin B6. B6 vitamers include, but are not limited to, pyridoxine (also called pyridoxol or PN), pyridoxal (PL), pyridoxamine (PM), the 5' phosphorylated derivatives of any of the three aforementioned compounds (PNP, PLP, 30 and PMP), and any derivative or related compound that can be converted to the active forms (PLP or PMP) in a test organism. Thus, for example, the acetate esters or other esters of any of the available hydroxyl groups of any of the aforementioned six compounds, and which are likely to be hydrolyzed by specific or non-specific esterases, are included in B₆ vitamers. Also, various salts, such as hydrochloride salts, of any of 35 the aforementioned compounds are included in B6 vitamers.

The term "B6 vitamer biosynthetic pathway" includes the biosynthetic pathway involving B6 vitamer biosynthetic enzymes (e.g., polypeptides encoded by

biosynthetic enzyme-encoding genes), compounds (e.g., precursors, substrates, intermediates or products), cofactors and the like utilized in the formation or synthesis of B6 vitamers. The term "B6 vitamer biosynthetic pathway" includes the biosynthetic pathway leading to the synthesis of B6 vitamers in a microorganism (e.g., *in vivo*) as well as the biosynthetic pathway leading to the synthesis of B6 vitamers *in vitro*.

5 A "biological assay for a B6 vitamer" includes, for example, any assay that is capable of quantifying B6 vitamer activity by measuring growth of an organism that requires the feeding of a B6 vitamer (*i.e.*, a compound that the fed organism can convert into PLP or PMP) for growth. Samples to be assayed are diluted serially in an
10 appropriate medium and fed to the appropriate organism. Standard curves are generated by serially diluting known amounts of PL, PN, or PM, and feeding these dilutions to the test organism. By comparing dilutions of the unknown samples to the standard curves, total B6 vitamer activity can be determined, for example as PL equivalents if PL was used to generate the standard curve.

15

Various aspects of the invention are described in further detail in the following subsections.

20 I. Genes Encoding Various B6 Vitamer Biosynthetic Enzymes

In one embodiment, the present invention features targeting or modifying various biosynthetic genes or enzymes of the B6 vitamer biosynthetic pathway. In particular, the invention features modifying various enzymatic activities associated with said pathways by modifying or altering the genes encoding said biosynthetic enzymes.

25 The term "gene", as used herein, includes a nucleic acid molecule (e.g., a DNA molecule or segment thereof) that, in an organism, can be separated from another gene or other genes, by intergenic DNA (*i.e.*, intervening or spacer DNA which naturally flanks the gene and/or separates genes in the chromosomal DNA of the organism). Alternatively, a gene may slightly overlap another gene (e.g., the 3' end of a first gene overlapping the 5' end of a second gene), said overlapping genes separated
30 from other genes by intergenic DNA. A gene may direct synthesis of an enzyme or other protein molecule (e.g., may comprise coding sequences, for example, a contiguous open reading frame (ORF) which encodes a protein) or may itself be functional in the organism. A gene in an organism, may be clustered in an operon, as defined herein, said operon being separated from other genes and/or operons by the intergenic DNA. An
35 "isolated gene", as used herein, includes a gene which is essentially free of sequences which naturally flank the gene in the chromosomal DNA of the organism from which the gene is derived (*i.e.*, is free of adjacent coding sequences which encode a second or

distinct protein, adjacent structural sequences or the like) and optionally includes 5' and 3' regulatory sequences, for example promoter sequences and/or terminator sequences.

In one embodiment, an isolated gene includes predominantly coding sequences for a protein (e.g., sequences which encode *Bacillus* proteins). In another embodiment, an

5 isolated gene includes coding sequences for a protein (e.g., for a *Bacillus* protein) and adjacent 5' and/or 3' regulatory sequences from the chromosomal DNA of the organism from which the gene is derived (e.g., adjacent 5' and/or 3' *Bacillus* regulatory sequences). Preferably, an isolated gene contains less than about 10 kb, 5 kb, 2 kb, 1 kb, 0.5 kb, 0.2 kb, 0.1 kb, 50 bp, 25 bp or 10 bp of nucleotide sequences that naturally flank

10 the gene in the chromosomal DNA of the organism from which the gene is derived.

The term "operon" includes at least two adjacent genes or ORFs, optionally overlapping in sequence at either the 5' or 3' end of at least one gene or ORF. The term "operon" includes a coordinated unit of gene expression that contains a promoter and possibly a regulatory element associated with one or more adjacent genes or ORFs (e.g., structural genes encoding enzymes, for example, biosynthetic enzymes). Expression of the genes (e.g., structural genes) can be coordinately regulated, for example, by regulatory proteins binding to the regulatory element or by anti-termination of transcription. The genes of an operon (e.g., structural genes) can be transcribed to give a single mRNA that encodes all of the proteins.

20 A "gene having a mutation" or "mutant gene" as used herein, includes a gene having a nucleotide sequence which includes at least one alteration (e.g., substitution, insertion, deletion) such that the polypeptide or protein encoded by said mutant exhibits an activity that differs from the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene. In one embodiment, a gene having a mutation

25 or mutant gene encodes a polypeptide or protein having an increased activity as compared to the polypeptide or protein encoded by the wild-type gene, for example, when assayed under similar conditions (e.g., assayed in microorganisms cultured at the same temperature). As used herein, an "increased activity" or "increased enzymatic activity" is one that is at least 5% greater than that of the polypeptide or protein encoded

30 by the wild-type nucleic acid molecule or gene, preferably at least 5-10% greater, more preferably at least 10-25% greater and even more preferably at least 25-50%, 50-75% or 75-100% greater than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene. Ranges intermediate to the above-recited values, e.g., 75-85%, 85-90%, 90-95%, are also intended to be encompassed by the present

35 invention. As used herein, an "increased activity" or "increased enzymatic activity" can also include an activity that is at least 1.25-fold greater than the activity of the polypeptide or protein encoded by the wild-type gene, preferably at least 1.5-fold

greater, more preferably at least 2-fold greater and even more preferably at least 3-fold, 4-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold or greater than the activity of the polypeptide or protein encoded by the wild-type gene.

In another embodiment, a gene having a mutation or mutant gene

5 encodes a polypeptide or protein having a reduced activity as compared to the polypeptide or protein encoded by the wild-type gene, for example, when assayed under similar conditions (e.g., assayed in microorganisms cultured at the same temperature). A mutant gene also can encode no polypeptide or have a reduced level of production of the wild-type polypeptide. As used herein, a "reduced activity" or "reduced enzymatic

10 activity" is one that is at least 5% less than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene, preferably at least 5-10% less, more preferably at least 10-25% less and even more preferably at least 25-50%, 50-75% or 75-100% less than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene. Ranges intermediate to the above-recited values, e.g., 75-85%, 15 85-90%, 90-95%, are also intended to be encompassed by the present invention. As used herein, a "reduced activity" or "reduced enzymatic activity" can also include an activity that has been deleted or "knocked out" (e.g., approximately 100% less activity than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene).

20 Activity can be determined according to any well accepted assay for measuring activity of a particular protein of interest. Activity can be measured or assayed directly, for example, measuring an enzymatic or biological activity of a protein isolated or purified from a cell or microorganism. Alternatively, an activity can be measured or assayed within a cell or macroorganism or in an extracellular medium. For example, assaying for a mutant gene (i.e., said mutant encoding a reduced enzymatic activity) can be accomplished by expressing the mutated gene in a microorganism, for example, a mutant microorganism in which the enzyme is temperature-sensitive, and assaying the mutant gene for the ability to complement a temperature sensitive (Ts) mutant for enzymatic activity. A mutant gene that encodes an "increased enzymatic

25 activity" can be one that complements the Ts mutant more effectively than, for example, a corresponding wild-type gene. A mutant gene that encodes a "reduced enzymatic activity" is one that complements the Ts mutant less effectively than, for example, a corresponding wild-type gene.

30 It will be appreciated by the skilled artisan that even a single substitution in a nucleic acid or gene sequence (e.g., a base substitution that encodes an amino acid change in the corresponding amino acid sequence) can dramatically affect the activity of an encoded polypeptide or protein as compared to the corresponding wild-type

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polypeptide or protein. A mutant gene (e.g., encoding a mutant polypeptide or protein), as defined herein, is readily distinguishable from a nucleic acid or gene encoding a protein homologue in that a mutant gene encodes a protein or polypeptide having an altered activity, optionally observable as a different or distinct phenotype in a

5 microorganism expressing said mutant gene or producing said mutant protein or polypeptide (i.e., a mutant microorganism) as compared to a corresponding microorganism expressing the wild-type gene. By contrast, a protein homologue has an identical or substantially similar activity, optionally phenotypically indiscernible when produced in a microorganism, as compared to a corresponding microorganism

10 expressing the wild-type gene. Accordingly it is not, for example, the degree of sequence identity between nucleic acid molecules, genes, protein or polypeptides that serves to distinguish between homologues and mutants, rather it is the activity of the encoded protein or polypeptide that distinguishes between homologues and mutants: homologues having, for example, low (e.g., 30-50% sequence identity) sequence

15 identity yet having substantially equivalent functional activities, and mutants, for example sharing 99% sequence identity yet having dramatically different or altered functional activities.

In a preferred embodiment, the genes of the present invention are derived from *Bacillus*. The term "derived from *Bacillus*" or "*Bacillus*-derived" includes a gene which is naturally found in microorganisms of the genus *Bacillus*. In another preferred embodiment, the genes of the present invention are derived from a microorganism selected from the group consisting of *Bacillus subtilis*, *Bacillus lenthimorbus*, *Bacillus lentinus*, *Bacillus firmus*, *Bacillus pantothenticus*, *Bacillus amylolyticus*, *Bacillus cereus*, *Bacillus circulans*, *Bacillus coagulans*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus thuringiensis*, *Bacillus halodurans*, and other Group 1 *Bacillus* species, for example, as characterized by 16S rRNA type. In another preferred embodiment, the gene is derived from *Bacillus brevis* or *Bacillus stearothermophilus*. In another preferred embodiment, the genes of the present invention are derived from a microorganism selected from the group consisting of *Bacillus licheniformis*, *Bacillus amylolyticus*, *Bacillus subtilis*, and *Bacillus pumilus*. In a particularly preferred embodiment, the gene is derived from *Bacillus subtilis* (e.g., is *Bacillus subtilis*-derived). The term "derived from *Bacillus subtilis*" or "*Bacillus subtilis*-derived" includes a gene which is naturally found in the microorganism *Bacillus subtilis*. Included within the scope of the present invention are *Bacillus*-derived genes (e.g., *B. subtilis*-derived genes), for example, *Bacillus* or *B. subtilis yaaD* or *yaaE* genes.

II. Recombinant Nucleic Acid Molecules and Vectors

The present invention further features recombinant nucleic acid molecules (e.g., recombinant DNA molecules) that include genes described herein (e.g., isolated genes), preferably *Bacillus* genes, more preferably *Bacillus subtilis* genes, even more preferably *Bacillus subtilis* B6 vitamer biosynthetic genes. The term "recombinant nucleic acid molecule" includes an isolated nucleic acid molecule (e.g., a DNA molecule) that has been altered, modified or engineered such that it differs in nucleotide sequence from the native or natural nucleic acid molecule from which the recombinant nucleic acid molecule was derived (e.g., by addition, deletion or substitution of one or more nucleotides). Preferably, a recombinant nucleic acid molecule (e.g., a recombinant DNA molecule) includes an isolated gene of the present invention operably linked to regulatory sequences. The phrase "operably linked to regulatory sequence(s)" means that the nucleotide sequence of the gene of interest is linked to the regulatory sequence(s) in a manner which allows for expression (e.g., enhanced, increased, constitutive, basal, attenuated, decreased or repressed expression) of the gene, preferably expression of a gene product encoded by the gene (e.g., when the recombinant nucleic acid molecule is included in a recombinant vector, as defined herein, and is introduced into a microorganism). A "recombinant organism" is any organism that contains a recombinant nucleic acid molecule.

The term "regulatory sequence" includes nucleic acid sequences that affect (e.g., modulate or regulate) expression of other nucleic acid sequences (i.e., genes). In one embodiment, a regulatory sequence is included in a recombinant nucleic acid molecule in a similar or identical position and/or orientation relative to a particular gene of interest as is observed for the regulatory sequence and gene of interest as it appears in nature, e.g., in a native position and/or orientation. For example, a gene of interest can be included in a recombinant nucleic acid molecule operably linked to a regulatory sequence which accompanies or is adjacent to the gene of interest in the natural organism (e.g., operably linked to "native" regulatory sequences (e.g., to the "native" promoter). Alternatively, a gene of interest can be included in a recombinant nucleic acid molecule operably linked to a regulatory sequence which accompanies or is adjacent to another (e.g., a different) gene in the natural organism. Alternatively, a gene of interest can be included in a recombinant nucleic acid molecule operably linked to a regulatory sequence from another organism. For example, regulatory sequences from other microbes (e.g., other bacterial regulatory sequences, bacteriophage regulatory sequences and the like) can be operably linked to a particular gene of interest.

In one embodiment, a regulatory sequence is a non-native or non-naturally-occurring sequence (e.g., a sequence which has been modified, mutated,

substituted, derivatized, deleted including sequences which are chemically synthesized). Preferred regulatory sequences include promoters, enhancers, termination signals, anti-termination signals, ribosome binding sites and other expression control elements (e.g., sequences to which repressors or inducers bind and/or binding sites for transcriptional and/or translational regulatory proteins, for example, in the transcribed mRNA). Such regulatory sequences are described, for example, in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989. Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in a microorganism (e.g., constitutive promoters and strong constitutive promoters), those which direct inducible expression of a nucleotide sequence in a microorganism (e.g., inducible promoters, for example, xylose inducible promoters) and those which attenuate or repress expression of a nucleotide sequence in a microorganism (e.g., attenuation signals or repressor sequences). It is also within the scope of the present invention to regulate expression of a gene of interest by removing or deleting regulatory sequences. For example, sequences involved in the negative regulation of transcription can be removed such that expression of a gene of interest is enhanced.

In one embodiment, a recombinant nucleic acid molecule of the present invention includes a nucleic acid sequence or gene that encodes at least one bacterial gene product (e.g., a B6 vitamer biosynthetic enzyme, e.g., the gene product of *yaaD* and/or *yaaE*) operably linked to a promoter or promoter sequence. Preferred promoters of the present invention include *Bacillus* promoters and/or bacteriophage promoters (e.g., bacteriophage which infect *Bacillus*). In one embodiment, a promoter is a *Bacillus* promoter, preferably a strong *Bacillus* promoter (e.g., a promoter associated with a biochemical housekeeping gene in *Bacillus* or a promoter associated with a glycolytic pathway gene in *Bacillus*). In another embodiment, a promoter is a bacteriophage promoter. In a preferred embodiment, the promoter is from the bacteriophage SP01. In a particularly preferred embodiment, a promoter is selected from the group consisting of *P₁₅*, *P₂₆*, or *P_{veg}* having for example, the following respective sequences:

30 GCTATTGACGACAGCTATGGITCACTGTCCACCAACCAAAACTGTGCTCAGT
ACCGCCAATATTTCTCCCTTGAGGGGTACAAAGAGGTGTCCCTAGAAGAGAT
CCACGCTGTGAAAAATTACAAAAAGGTATTGACTTCCCTACAGGGTGT
GTAATAATTAAATTACAGGCAGGGCAACCCGCCGT (SEQ ID NO:9),
GCCTACCTAGCTTCCAAGAAAGATATCCTAACAGCACAAAGAGCGGAAAGAT
35 GTTTGTTCTACATCCAGAACAAACCTCTGCTAAAATTCCCTGAAAAATTTCG
AAAAAGTTGTTGACTTATCTACAAGGTGTGGTATAATAATCTTAACAAACAG
CAGGACGC (SEQ ID NO:10); and

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GAGGAATCATAGAATTGTCAAAATAATTGACAACGTCTTATTAAC
GTTGATATAATTAAATTITATTGACAAAAATGGGCTCGTGTACAATA
AATGTAGTGAGGTGGATGCAATG (SEQ ID NO:11). Additional preferred
5 promoters include *tef* (the translational elongation factor (TEF) promoter) and *pyc* (the
pyruvate carboxylase (PYC) promoter), which promote high level expression in *Bacillus*
(e.g., *Bacillus subtilis*). Additional preferred promoters, for example, for use in Gram
positive microorganisms include, but are not limited to, *amy* and *SPO2* promoters.
Additional preferred promoters, for example, for use in Gram negative microorganisms
10 include, but are not limited to, *tac*, *trp*, *tet*, *trp-tet*, *lpp*, *lac*, *lpp-lac*, *lacIQ*, T7, T5, T3,
gal, *trc*, *ara*, SP6, λ-PR or λ-PL.

In another embodiment, a recombinant nucleic acid molecule of the present invention includes a terminator sequence or terminator sequences (e.g., transcription terminator sequences). The term "terminator sequences" includes regulatory sequences that serve to terminate transcription of mRNA. Terminator sequences (or tandem transcription terminators) can further serve to stabilize mRNA (e.g., by adding structure to mRNA), for example, against nucleases.

15 In yet another embodiment, a recombinant nucleic acid molecule of the present invention includes sequences which allow for detection of the vector containing said sequences (i.e., detectable and/or selectable markers), for example, genes that encode antibiotic resistance or sequences that overcome auxotrophic mutations, for example, *trpC*, fluorescent markers, drug markers, and/or colorimetric markers (e.g., *lacZ*/β-galactosidase). In yet another embodiment, a recombinant nucleic acid molecule of the present invention includes an artificial ribosome binding site (RBS) or a sequence that becomes transcribed into an artificial RBS. The term "artificial ribosome binding 20 site (RBS)" includes a site within an mRNA molecule (e.g., coded within DNA) to which a ribosome binds (e.g., to initiate translation) which differs from a native RBS (e.g., a RBS found in a naturally-occurring gene) by at least one nucleotide. Preferred artificial RBSs include about 5-6, 7-8, 9-10, 11-12, 13-14, 15-16, 17-18, 19-20, 21-22, 25-26, 27-28, 29-30 or more nucleotides of which about 1-2, 3-4, 5-6, 7-8, 9-10, 30 11-12, 13-15 or more differ from the native RBS (e.g., the native RBS of a gene of interest, for example, the native *yaaD* RBS
GAAATCATATAACTATACCTTGATTAGGGGGACCAAGAAATG
(SEQ ID NO:12) or the native *yaaE* RBS
CAAGAACGCCGCTGGTAAGAACATAGGAGCGCTGCTGACATG (SEQ ID
35 NO:13)).

Preferably, nucleotides that differ are substituted such that they are identical to one or more nucleotides of an ideal RBS when optimally aligned for

comparisons. Artificial RBSs can be used to replace the naturally-occurring or native RBSs associated with a particular gene. Artificial RBSs preferably increase translation of a particular gene. Preferred artificial RBSs (e.g., RBSs for increasing the translation of *yaaE*, for example, of *B. subtilis*) are set forth in Table 1, below.

5

Table 1: Preferred Ribosome Binding Sites

	10	20	SEQ ID NO:
10		— — —	
Native_yaaD	—GAAATCATATAACTATACCTTGATTAGGGGACC-	AAGAAATG	12
Native_yaaE	CAAGAACGGCGCTGGTAAGAACAT	—AGGAGCGCTGCTGACATG	13
IDEAL_RBS	TCTAGAAAGG	—AGGTG—A—	14
RBS1	TCTAGAAGG	—AGGAG—	15
RBS2	TCTAGAGG	—AGGAG—	16
RBS101	—TAAGAACAA	—AGGAGGAGAGCTGACATG	17
RBS103	—TAAGAAGAA	—AGGAGGTGAGCTGACATG	18
RBS102	—TAAGAACAG	—AGGAGGAGAGCTGACATG	19

20

The present invention further features vectors (e.g., recombinant vectors) that include nucleic acid molecules (e.g., genes or recombinant nucleic acid molecules comprising said genes) as described herein. The term "recombinant vector" includes a vector (e.g., plasmid, phage, phasmid, virus, cosmid or other purified nucleic acid vector) that has been altered, modified or engineered such that it contains greater, fewer or different nucleic acid sequences than those included in the native or natural nucleic acid molecule from which the recombinant vector was derived. Preferably, the recombinant vector includes a biosynthetic enzyme-encoding gene or recombinant nucleic acid molecule including said gene, operably linked to regulatory sequences, for example, promoter sequences, terminator sequences and/or artificial ribosome binding sites (RBSs), as defined herein.

25

In another embodiment, a recombinant vector of the present invention includes sequences that enhance replication in bacteria (e.g., replication-enhancing sequences). In one embodiment, replication-enhancing sequences are derived from *E. coli*. In another embodiment, replication-enhancing sequences are derived from pBR322. In another embodiment, replication-enhancing sequences are derived from pSC101.

30

In yet another embodiment, a recombinant vector of the present invention includes antibiotic resistance sequences. The term "antibiotic resistance sequences" includes sequences which promote or confer resistance to antibiotics on the host organism (e.g., *Bacillus*). In one embodiment, the antibiotic resistance sequences are selected from the group consisting of *cat* (chloramphenicol resistance) sequences, *tet* (tetracycline resistance) sequences, *erm* (erythromycin resistance) sequences, *neo*

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(neomycin resistance) sequences, *kan* (kanamycin resistance) and *spec* (spectinomycin resistance) sequences. Recombinant vectors of the present invention can further include homologous recombination sequences (e.g., sequences designed to allow recombination of the gene of interest into the chromosome of the host organism). For example, *bpr*, 5 *vpr*, and/or *amyE* sequences can be used as homology targets for recombination into the host chromosome. It will further be appreciated by one of skill in the art that the design of a vector can be tailored depending on such factors as the choice of microorganism to be genetically engineered, the level of expression of gene product desired and the like.

10

III. Recombinant Microorganisms

The present invention further features microorganisms, i.e., recombinant microorganisms, that include vectors or genes (e.g., wild-type and/or mutated genes) as described herein. As used herein, the term "recombinant microorganism" includes a microorganism (e.g., bacteria, yeast cell, fungal cell, etc.) that has been genetically altered, modified or engineered (e.g., genetically engineered) such that it exhibits an altered, modified or different genotype and/or phenotype (e.g., when the genetic modification affects coding nucleic acid sequences of the microorganism) as compared to the naturally-occurring microorganism from which it was derived.

In one embodiment, a recombinant microorganism of the present 20 invention is a Gram positive organism (e.g., a microorganism which retains basic dye, for example, crystal violet, due to the presence of a Gram-positive wall surrounding the microorganism). In a preferred embodiment, the recombinant microorganism is a microorganism belonging to a genus selected from the group consisting of *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*. In a more preferred 25 embodiment, the recombinant microorganism is of the genus *Bacillus*. In another preferred embodiment, the recombinant microorganism is selected from the group consisting of *Bacillus subtilis*, *Bacillus lenticorbus*, *Bacillus lentinus*, *Bacillus firmus*, *Bacillus pantothenicus*, *Bacillus amyloliquefaciens*, *Bacillus cereus*, *Bacillus circulans*, *Bacillus coagulans*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, 30 *Bacillus thuringiensis*, *Bacillus halodurans*, and other Group 1 *Bacillus* species, for example, as characterized by 16S rRNA type. In another preferred embodiment, the recombinant microorganism is *Bacillus brevis* or *Bacillus stearothermophilus*. In another preferred embodiment, the recombinant microorganism is selected from the 35 group consisting of *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus subtilis*, and *Bacillus pumilus*.

In another embodiment, the recombinant microorganism is a Gram negative (excludes basic dye) organism. In a preferred embodiment, the recombinant

microorganism is a microorganism belonging to a genus selected from the group consisting of *Salmonella*, *Escherichia*, *Klebsiella*, *Serratia*, and *Proteus*. In a more preferred embodiment, the recombinant microorganism is of the genus *Escherichia*. In an even more preferred embodiment, the recombinant microorganism is *Escherichia coli*. In another embodiment, the recombinant microorganism is *Saccharomyces* (e.g., *S. cerevisiae*).

A preferred "recombinant" microorganism of the present invention is a microorganism having a deregulated B6 vitamer biosynthesis pathway or enzyme. The term "deregulated" or "deregulation" includes the alteration or modification of at least one gene in a microorganism that encodes an enzyme in a biosynthetic pathway, such that the level or activity of the biosynthetic enzyme in the microorganism is altered or modified. Preferably, at least one gene that encodes an enzyme in a biosynthetic pathway is altered or modified such that the gene product is enhanced or increased. The phrase "deregulated pathway" can also include a biosynthetic pathway in which more than one gene that encodes an enzyme in a biosynthetic pathway is altered or modified such that the level or activity of more than one biosynthetic enzyme is altered or modified. The ability to "deregulate" a pathway (e.g., to simultaneously deregulate more than one gene in a given biosynthetic pathway) in a microorganism in some cases arises from the particular phenomenon of microorganisms in which more than one enzyme (e.g., two or three biosynthetic enzymes) are encoded by genes occurring adjacent to one another on a contiguous piece of genetic material termed an "operon" (defined herein). Due to the coordinated regulation of genes included in an operon, alteration or modification of the single promoter and/or regulatory element can result in alteration or modification of the expression of more than one gene product encoded by the operon. Alteration or modification of the regulatory element can include, but is not limited to removing the endogenous promoter and/or regulatory element(s), adding strong promoters, inducible promoters or multiple promoters or removing regulatory sequences such that expression of the gene products is modified, modifying the chromosomal location of the operon, altering nucleic acid sequences adjacent to the operon or within the operon such as a ribosome binding site, increasing the copy number of the operon, modifying proteins (e.g., regulatory proteins, suppressors, enhancers, transcriptional activators and the like) involved in transcription of the operon and/or translation of the gene products of the operon, or any other conventional means of deregulating expression of genes routine in the art (including but not limited to use of antisense nucleic acid molecules, for example, to block expression of repressor proteins). Deregulation can also involve altering the coding region of one or more genes

to yield, for example, an enzyme that is feedback resistant or has a higher or lower specific activity.

In another preferred embodiment, a recombinant microorganism is designed or engineered such that at least one B6 vitamer biosynthetic enzyme, is overexpressed. The term "overexpressed" or "overexpression" includes expression of a gene product (e.g., a biosynthetic enzyme) at a level greater than that expressed prior to manipulation of the microorganism or in a comparable microorganism which has not been manipulated. In one embodiment, the microorganism can be genetically designed or engineered to overexpress a level of gene product greater than that expressed in a comparable microorganism which has not been engineered.

Genetic engineering can include, but is not limited to, altering or modifying regulatory sequences or sites associated with expression of a particular gene (e.g., by adding strong promoters, inducible promoters or multiple promoters or by removing regulatory sequences such that expression is constitutive), modifying the chromosomal location of a particular gene, altering nucleic acid sequences adjacent to a particular gene such as a ribosome binding site, increasing the copy number of a particular gene, modifying proteins (e.g., regulatory proteins, suppressors, enhancers, transcriptional activators and the like) involved in transcription of a particular gene and/or translation of a particular gene product, or any other conventional means of deregulating expression of a particular gene routine in the art (including but not limited to use of antisense nucleic acid molecules, for example, to block expression of repressor proteins). Genetic engineering can also include deletion of a gene, for example, to block a pathway or to remove a repressor. In embodiments featuring microorganisms having deleted genes, the skilled artisan will appreciate that at least low levels of certain compounds may be required to be present in or added to the culture medium in order that the viability of the microorganism is not compromised. Often, such low levels are present in complex culture media as routinely formulated. Moreover, in processes featuring culturing microorganisms having deleted genes cultured under conditions such that commercially or industrially attractive quantities of product are produced, it may be necessary to supplement culture media with slightly increased levels of certain compounds.

In another embodiment, the microorganism can be physically or environmentally manipulated to overexpress a level of gene product greater than that expressed prior to manipulation of the microorganism or in a comparable microorganism which has not been manipulated. For example, a microorganism can be treated with or cultured in the presence of an agent known or suspected to increase transcription of a particular gene and/or translation of a particular gene product such that transcription

and/or translation are enhanced or increased. Alternatively, a microorganism can be cultured at a temperature selected to increase transcription of a particular gene and/or translation of a particular gene product such that transcription and/or translation are enhanced or increased.

5

IV. Culturing and Fermenting Recombinant Microorganisms

The term "culturing" includes maintaining and/or growing a living microorganism of the present invention (e.g., maintaining and/or growing a culture or strain). In one embodiment, a microorganism of the invention is cultured in liquid media. In another embodiment, a microorganism of the invention is cultured in solid media or semi-solid media. In a preferred embodiment, a microorganism of the invention is cultured in media (e.g., a sterile, liquid media) comprising nutrients essential or beneficial to the maintenance and/or growth of the microorganism (e.g., carbon sources or carbon substrate, for example carbohydrate, hydrocarbons, oils, fats, fatty acids, organic acids, and alcohols; nitrogen sources, for example, peptone, yeast extracts, meat extracts, malt extracts, soy flour, urea, ammonium sulfate, ammonium chloride, ammonium nitrate and ammonium phosphate; phosphorus sources, for example, phosphoric acid, sodium and potassium salts thereof; trace elements, for example, magnesium, iron, manganese, calcium, copper, zinc, boron, molybdenum, and/or cobalt salts; as well as growth factors such as amino acids, vitamins, and the like).

Preferably, microorganisms of the present invention are cultured under controlled pH. The term "controlled pH" includes any pH which results in production of the desired product. In one embodiment microorganisms are cultured at a pH of about 7. In another embodiment, microorganisms are cultured at a pH of between 6.0 and 8.5. The desired pH may be maintained by any number of methods known to those skilled in the art.

Also preferably, microorganisms of the present invention are cultured under controlled aeration. The term "controlled aeration" includes sufficient aeration (e.g., oxygen) to result in production of the desired product. In one embodiment, aeration is controlled by regulating oxygen levels in the culture, for example, by regulating the amount of oxygen dissolved in culture media. Preferably, aeration of the culture is controlled by agitating the culture. Agitation may be provided by a propeller or similar mechanical agitation equipment, by revolving or shaking the culture vessel (e.g., tube or flask) or by various pumping equipment. Aeration may be further controlled by the passage of sterile air or oxygen through the medium (e.g., through the

fermentation mixture). Also preferably, microorganisms of the present invention are cultured without excess foaming (e.g., via addition of antifoaming agents).

Moreover, microorganisms of the present invention can be cultured under controlled temperatures. The term "controlled temperature" includes any temperature

- 5 which results in production of the desired product (e.g., a B6 vitamer). In one embodiment, controlled temperatures include temperatures between 15°C and 95°C. In another embodiment, controlled temperatures include temperatures between 15°C and 70°C. Preferred temperatures are between 20°C and 55°C, more preferably between 30°C and 50°C.

- 10 Microorganisms can be cultured (e.g., maintained and/or grown) in liquid media and preferably are cultured, either continuously or intermittently, by conventional culturing methods such as standing culture, test tube culture, shaking culture (e.g., rotary shaking culture, shake flask culture, etc.), aeration spinner culture, or fermentation. In a preferred embodiment, the microorganisms are cultured in shake flasks. In a more preferred embodiment, the microorganisms are cultured in a fermentor (e.g., a fermentation process). Fermentation processes of the present invention include, but are not limited to, batch, fed-batch and continuous processes or methods of fermentation.
- 15 The phrase "batch process" or "batch fermentation" refers to a closed system in which the composition of media, nutrients, supplemental additives and the like is set at the beginning of the fermentation and not subject to alteration during the fermentation, however, attempts may be made to control such factors as pH and oxygen concentration to prevent excess media acidification and/or microorganism death. The phrase "fed-batch process" or "fed-batch" fermentation refers to a batch fermentation with the exception that one or more substrates or supplements are added (e.g., added in
- 20 increments or continuously) as the fermentation progresses. The phrase "continuous process" or "continuous fermentation" refers to a system in which a defined fermentation media is added continuously to a fermentor and an equal amount of used or "conditioned" media is simultaneously removed, preferably for recovery of the desired product (e.g., a B6 vitamer). A variety of such processes have been developed and are well-known in the art.
- 25
- 30

- 35 The phrase "culturing under conditions such that a desired compound is produced" includes maintaining and/or growing microorganisms under conditions (e.g., temperature, pressure, pH, duration, etc.) appropriate or sufficient to obtain production of the desired compound or to obtain desired yields of the particular compound being produced. For example, culturing is continued for a time sufficient to produce the desired amount of a compound (e.g., a B6 vitamer). Preferably, culturing is continued for a time sufficient to substantially reach suitable production of the compound (e.g., a

time sufficient to reach a suitable concentration of a B6 vitamer). In one embodiment, culturing is continued for about 12 to 24 hours. In another embodiment, culturing is continued for about 24 to 36 hours, 36 to 48 hours, 48 to 72 hours, 72 to 96 hours, 96 to 120 hours, 120 to 144 hours, or greater than 144 hours. The methodology of the present invention can further include a step of recovering a desired compound (e.g., a B6 vitamer). The term "recovering" a desired compound includes extracting, harvesting, isolating or purifying the compound from culture media. Recovering the compound can be performed according to any conventional isolation or purification methodology known in the art including, but not limited to, treatment with a conventional resin (e.g., 5 anion or cation exchange resin, non-ionic adsorption resin, etc.), treatment with a conventional adsorbent (e.g., activated charcoal, silicic acid, silica gel, cellulose, alumina, etc.), alteration of pH, solvent extraction (e.g., with a conventional solvent such as an alcohol, ethyl acetate, hexane and the like), dialysis, filtration, concentration, crystallization, recrystallization, pH adjustment, lyophilization and the like. For 10 example, a compound can be recovered from culture media by first removing the microorganisms from the culture. The resulting solutions are then passed through or over a cation exchange resin to remove cations and/or through or over an anion exchange resin to purify or concentrate the desired product. The resulting compound can subsequently be converted to a salt (e.g., a chloride or sulfate salt) by ion exchange.

15 Preferably, a desired compound of the present invention is "extracted," "isolated" or "purified" such that the resulting preparation is substantially free of other media components (e.g., free of media components and/or fermentation byproducts). The language "substantially free of other media components" includes preparations of the desired compound in which the compound is separated from media components or 20 fermentation byproducts of the culture from which it is produced. In one embodiment, the preparation has greater than about 80% (by dry weight) of the desired compound (e.g., less than about 20% of other media components or fermentation byproducts), more preferably greater than about 90% of the desired compound (e.g., less than about 10% of other media components or fermentation byproducts), still more preferably greater than 25 about 95% of the desired compound (e.g., less than about 5% of other media components or fermentation byproducts), and most preferably greater than about 98-99% desired compound (e.g., less than about 1-2% other media components or fermentation byproducts). When the desired compound has been derivatized to a salt, the compound is preferably further free of chemical contaminants associated with the 30 formation of the salt. When the desired compound has been derivatized to an alcohol, the compound is preferably further free of chemical contaminants associated with the formation of the alcohol.

35

In an alternative embodiment, the desired compound is not purified from the microorganism, for example, when the microorganism is biologically non-hazardous (e.g., safe). For example, the entire culture (or culture supernatant) can be used as a source of product (e.g., crude product). In one embodiment, the culture (or culture supernatant) is used without modification. In another embodiment, the culture (or culture supernatant) is concentrated. In yet another embodiment, the culture (or culture supernatant) is dried or lyophilized.

5 Preferably, a production method of the present invention results in production of the desired compound, e.g., a B6 vitamer, at a significantly high yield.

10 10 The phrase "significantly high yield" includes a level of production or yield which is sufficiently elevated or above what is usual for comparable production methods, for example, which is elevated to a level sufficient for commercial production of the desired product (e.g., production of the product at a commercially feasible cost). In one embodiment, the invention features a production method that includes culturing a recombinant microorganism under conditions such that the desired product (e.g., a B6 vitamer) is produced at a level greater than 5 mg/L. In another embodiment, the invention features a production method that includes culturing a recombinant microorganism under conditions such that the desired product (e.g., a B6 vitamer) is produced at a level greater than 10 mg/L. In another embodiment, the invention features a production method that includes culturing a recombinant microorganism under conditions such that the desired product (e.g., a B6 vitamer) is produced at a level greater than 150 mg/L.

15 20 25 30 35

Depending on the biosynthetic enzyme or combination of biosynthetic enzymes manipulated, it may be desirable or necessary to provide (e.g., feed) microorganisms of the present invention at least one biosynthetic precursor such that the desired compound or compounds are produced. The term "biosynthetic precursor" or "precursor" includes an agent or compound which, when provided to, brought into contact with, or included in the culture medium of a microorganism, serves to enhance or increase biosynthesis of the desired product. In one embodiment, the biosynthetic precursor or precursor is glutamine. In another embodiment, the biosynthetic precursor or precursor is ribose. The amount of glutamine or ribose added is preferably an amount that results in a concentration in the culture medium sufficient to enhance productivity of the microorganism (e.g., a concentration sufficient to enhance production of a B6 vitamer). The term "excess ribose or glutamine" includes ribose or glutamine levels increased or higher than those routinely utilized for culturing the microorganism in

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question. For example, culturing the *Bacillus* microorganisms described in the instant Examples is routinely done in the presence of about 0-5 g/L ribose or glutamine. Accordingly, excess ribose or glutamine levels can include levels of about 5-10 g/L or more preferably about 5-20 g/L ribose or glutamine. Biosynthetic precursors of the
5 present invention can be added in the form of a concentrated solution or suspension (e.g., in a suitable solvent such as water or buffer) or in the form of a solid (e.g., in the form of a powder). Moreover, biosynthetic precursors of the present invention can be added as a single aliquot, continuously or intermittently over a given period of time.

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This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patents and published patent applications cited throughout this application are incorporated herein by reference.

15

EXAMPLES

EXAMPLE 1: Biological assay for B6 vitamers using *Saccharomyces uvarum*.

Quantitation of B6 vitamers in supernatants of cultures of micro-
5 organisms or extracts of organisms that have been genetically modified to increase production of B6 vitamers is conveniently done using *Saccharomyces uvarum* (formerly and still often named *S. carlsbergensis*) strain ATCC 9080 as the indicator strain or test organism. The method is essentially that described in the Difco Manual (1984, Difco Laboratories, Detroit, MI, 10th Edition, pp. 1104-1106), with the modification that 50
10 mg/liter of streptomycin sulfate is added to the liquid growth medium for the test organism. However, any other appropriate indicator organism may be used, together with a medium that is appropriate for that organism that is free of B6 vitamers. For example, an *E. coli* *pdxB* mutant can be used in a standard minimal medium that is well known in the art, such as M9 glucose minimal medium (Miller, J., (1972) Experiments
15 in Molecular Genetics, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

When using *S. uvarum* strain ATCC 9080 as the indicator strain, Bacto Pyridoxine Y Medium (Difco Laboratories, available through VWR Scientific, Inc.), supplemented with 50 mg/liter streptomycin sulfate, is used for the serial dilutions, and PN, PL, or PM is used to generate the standard curve. The responses to these three
20 standard compounds are almost identical to each other with *S. uvarum* strain ATCC 9080 (Figure 3).

EXAMPLE 2: Deletion of a portion of the *yaaDE* operon in *B. subtilis*.

The *SOR* and *SNO* genes of *Cercospora nicotianae* were originally
25 identified by mutations that lead to hypersensitivity to singlet oxygen-generating reagents (Ehrenshaft, M., et al. (1999) *Proc. Natl. Acad. Sci. USA* 96: 9347-9378). Mutations in either of these genes also lead to PL auxotrophy. The protein sequences obtained from translation of the *SOR* and *SNO* open reading frames were used as homology probes to search through the *B. subtilis* genome sequence using the BLAST
30 homology search program of the Subtilist website. The *SOR* protein was significantly homologous to the *YaaD* protein, and the *SNO* protein was significantly homologous to the *YaaE* protein. Moreover, the genes encoding the *YaaD* and *YaaE* proteins (namely *yaaD* and *yaaE*) occur adjacent to each other on the *B. subtilis* chromosome as a two gene operon.

35 General methods for growth, storage, transformation, and molecular biology of *B. subtilis* strains are given in Harwood, C., and Cutting, S. (1990), Molecular Biological Methods for *Bacillus*, John Wiley and Sons, New York, NY, hereby

incorporated in its entirety by reference. The *yaaDE* operon DNA sequence was amplified using the Polymerase Chain Reaction (PCR) with Pfu Turbo DNA polymerase (Stratagene, Inc., used according to the manufacturer's instructions). The DNA primers used were RY395 (SEQ ID NO:1) and RY396 (SEQ ID NO:2). RY395, the upstream 5 primer, introduces an *XbaI* site and artificial ribosome binding site. RY396, the downstream primer, introduces a *BamHI* site. The template DNA was chromosomal DNA isolated from wild type *B. subtilis* strain PY79. The blunt ended PCR product was ligated into the *EcoRV* site of pGEM5Zf(+) (Promega, Inc.) to give plasmid pAN368. Next, a gram positive chloramphenicol resistance gene on a blunt DNA fragment was 10 ligated into pAN368 that had been cut with *HpaI*, to give plasmid pDX1F (SEQ ID NO:5, Figure 4). pDX1F therefore is deleted for a portion of *yaaD* and a portion of *yaaE*. pDX1F was used to transform wild type *B. subtilis* strain PY79 to 5 mg/liter chloramphenicol resistance, and a double crossover event was confirmed using PCR and the same primers used to clone *yaaDE*. The resulting strain was named PX1.

15 PX1 was able to grow on Spizizen's minimal medium with trace elements (SMM) (Harwood, C., and Cutting, S. (1990) Molecular Biological Methods for *Bacillus*, John Wiley and Sons, New York, NY, pp. 548-549) supplemented with 2 µM pyridoxal HCl (Sigma-Aldrich Chemical Co.), but it did not grow without the supplement. Thus it was established that at least one of *yaaD* or *yaaE* is required for 20 PLP synthesis in *B. subtilis*.

EXAMPLE 3: Deletion of *yhaF* in *B. subtilis*.

The protein sequence of the *E. coli* *pdxF* gene was used as a probe to search the *B. subtilis* genome as described in Example 1. The only significant homolog 25 was *yhaF*. In a fashion similar to that of Example 1, the *yhaF* was cloned and deleted from the chromosome of PY79 using plasmid pDX11F (SEQ ID NO:6, Figure 5), to give strain PX11. The PCR primers used to clone *yhaF* were RY407 (SEQ ID NO:3) and RY408 (SEQ ID NO:4). The restriction sites used for insertion of the antibiotic resistance gene were the *PshA1* and *EheI* sites in the *yhaF* coding region. PX11 is a 30 serine auxotroph, but not a PL auxotroph. By comparison to *E. coli*, it appears that *yhaF* functions in serine synthesis and probably encodes the equivalent of *SerC*, but that the YhaF protein is not required for PLP synthesis in *B. subtilis*. Therefore, it is established that sequence homology does not necessarily imply functional homology.

35 **EXAMPLE 4: Overexpression of the *yaaDE* operon in *B. subtilis*.**

The *XbaI* to *BamHI* fragment from pAN368 that contains the *yaaDE* operon and artificial ribosome binding site was inserted into either of two expression

vectors, to yield plasmids pDX14R (SEQ ID NO:7) and pDX17R (SEQ ID NO:8), respectively. In pDX14R and pDX17R, the *yaaDE* operon is expressed from the strong constitutive *B. subtilis* phage SP01 promoters, *P₂₆* and *P₁₅*, respectively (see Figures 6 and 7).

5 pDX14R and pDX17R were each transformed into wild type *B. subtilis* strain PY79, selecting for chloramphenicol resistance. The plasmids integrate into the chromosome at the *yaaDE* locus by single crossover. The resulting strains were named PX14 and PX17, respectively.

10 PX14 and PX17 were grown for 48 hours at 37°C in 5 ml test tube cultures in a roller drum at about 100 rotations per minute. The culture medium was SVY (20 g Difco Veal Infusion Broth, 5 g Difco Yeast Extract, 2 g ammonium sulfate, 5 g sodium glutamate, and 30 g glucose per liter, buffered with 200 mM potassium phosphate, pH 7.0). Cells were removed by centrifugation followed by sterile filtration (Millipore 0.45 micron), and the supernatant solutions were assayed for PL equivalents 15 using the biological assay described in Example 1. The parent strain, PY79 was grown and processed in similar fashion as a control. The uncultured SVY medium was assayed as another control, since it was likely that the SVY medium contained a measurable level of B6 vitamers. The results are shown in Table 2, below.

20 **Table 2:** Production of B6 vitamers by *Bacillus subtilis* derivatives in 48 hour test tube cultures grown in SVY

Strain	Cassette	Integration Target	OD ₆₀₀	Total B6 Vitamers ¹ mg/liter	Net B6 Vitamers ² mg/liter
PX14	<i>P₂₆yaaDE</i>	<i>yaaDE</i>	17	7.2	7.0
PX17	<i>P₁₅yaaDE</i>	<i>yaaDE</i>	17	4.9	4.7
PX1	<i>AyaaDE</i>	<i>yaaDE</i>	8	0.4	0.2
PY79	-	-	19	0.8	0.6
(Medium)	-	-	0.08	0.2	(0)

¹ Sum of PN, PL, PM, and derivatives thereof that can be utilized by pyridoxine indicator strain *S. carlbergensis* as a source of vitamin B6 for growth.

25 ² Calculated by subtracting the amount assayed in the medium.

After subtracting the B6 vitamers contained in the medium, strain PX14 produced 7.0 mg/liter PL equivalents, while the parent PY79 produced only 0.6 mg/liter of PL equivalents. Thus, expression of the *yaaDE* operon has been shown to be rate 30 limiting for B6 vitamer production in *B. subtilis*. Moreover, a genetically modified

- 25 -

strain, where this rate limiting step was enhanced, produced more than a ten-fold increase in B6 vitamer secretion compared to that of the parent.

5 **EXAMPLE 5: Complementation of *E. coli* *pdx* mutants by plasmids that express the *B. subtilis* *yaaDE* operon.**

Plasmid pDX14R, described above in Example 4, was used to transform various *E. coli* strains that contained mutations that lacked function in each of the known genes involved in PLP biosynthesis (except for *dxs*, which is an essential gene for *E. coli*). The selection was for resistance to 250 mg/liter ampicillin. Each transformant 10 was then tested for growth on minimal medium (SMM with 0.5 % glucose, see Example 2) supplemented with 100 mg/liter serine, and compared to growth of its respective untransformed parent on the same medium. All mutations tested were complemented by pDX14R. Specifically, *pdxA*, *pdxB*, *pdxF*, *pdxJ*, and *pdxH*, were all complemented by pDX14R. Therefore, expression of the *B. subtilis* *yaaDE* operon in *E. coli* is sufficient 15 for PLP biosynthesis, even in the absence of any one of the above functional *pdx* genes. Several important and unexpected conclusions or inferences can be drawn from these results. First, the substrate(s) for the enzyme(s) encoded by *yaaDE* must be present in *E. coli*, even when a biosynthetic intermediate normally used to make PLP is absent or greatly reduced. Second, PNP or PLP is possibly the product of the enzyme(s) encoded 20 by *yaaDE*. Third, since an early block in the *E. coli* PLP biosynthetic pathway (for example that in a *pdxB* mutant) does not prevent *yaaDE* from complementation, the substrates for the enzyme(s) encoded by *yaaDE* are not likely to be the same as for the last step in PNP or PLP synthesis in wild type *E. coli*. These unexpected results lead to the possibility of producing B6 vitamers using *B. subtilis* *yaaDE* or the homologous 25 genes from another organism (for example, but not limited to, *SOR* and *SNO* from *Cercospora nicotianae* or *PDX1* and *PDX2* from *S. cerevisiae*) in a heterologous host species, including, but not limited to, *E. coli* and *Oryza sativa*.

30 **EXAMPLE 6: Overexpression of the *yaaDE* operon in *E. coli*.**

Plasmids pDX14R and pDX17R were transformed into *E. coli* strain DH5 α (New England Biolabs), selecting for ampicillin resistance. The transformants were grown for 48 hours in 5 ml test tube cultures at 37°C, and the supernatants were worked up as in Example 3. The assay results for PL equivalents are shown in Table 3, below.

Table 3: Production of B6 vitamers by *Escherichia coli* harboring plasmids containing engineered *Bacillus subtilis* genes¹

Strain	Plasmid Cassette	OD ₆₀₀	Total B6 Vitamers ² mg/liter	Net B6 Vitamers ³ mg/liter
DH5α	<i>P₂yaaDE</i>	7.6	3.2	3.1
DH5α	<i>P₁₅yaaDE</i>	8.2	3.2	3.1
DH5α		9	0.1	(0)

¹*E. coli* test tube cultures are grown in SVY for 48 hours.

²Sum of PN, PL, PM, and derivatives thereof that can be utilized by pyridoxine indicator strain *S. carlbergensis* as a source of vitamin B6 for growth.

³Calculated by subtracting the amount assayed in DH5α not containing plasmid.

Thus it has been shown that the *yaaD* and *yaaE* genes can be expressed in a heterologous host strain, and B6 vitamers can still be overproduced. By extension of this approach, the *yaaD* and *yaaE* genes of *B. subtilis* can be overexpressed in any organism where an overexpression system exists, and in the resulting strains, B6 vitamers will be overproduced. Overproduction of the rate limiting enzyme for B6 vitamer production in any organism that is capable of producing B6 vitamers will lead to overproduction of B6 vitamers.

The YaaD and YaaE protein sequences were used as probes to search the NCBI database for homologs in plants using the BLAST™ program which can be found at the National Center for Biotechnology Information website (Altschul S.F (1990) *J. Mol. Biol.* 215(3):403-10). Several homologs of YaaD were found in several genera of plants, including *Arabidopsis*, *Oryza*, *Ginkgo*, *Hevea*, *Phaseolus*, and *Stellaria*. Two homologs of YaaE were found in *Arabidopsis thaliana*. However, no homologs of *pdxA* and *pdxJ* were found. Therefore the plant kingdom appears to use the Type B Pathway for B6 vitamer biosynthesis. Thus for example, overexpression of the YaaD homolog (GenBank accession number AAL73561) from *Oryza sativa* (rice), and the *A. thaliana* homolog of YaaE (GenBank accession number AB011483) together in a plant using methods well known in the art, such as expression from the Cauliflower Mosaic Virus 35S promoter, will lead to overproduction of B6 vitamers in that plant.

EXAMPLE 7: Other routes to increasing the activity of enzymes involved in B6 vitamer synthesis.

The overexpression of the *yaaDE* operon leads to an increase in the amount of the encoded enzyme(s), which in turn leads to an increase in the total activity of said enzyme(s). Increase in this activity leads to an increase in the production B6 vitamer. Other methods can be used to increase the activity of the relevant enzyme(s).

under conditions of B6 vitamer production. For example, in addition to increasing the amount of a relevant enzyme(s), the total activity of the relevant enzyme(s) can be increased by mutating the gene(s) to increase the specific activity of the enzyme(s), and/or by mutating the gene(s) to encode a feedback resistant variant of the enzyme(s).

5 Such desirable mutations can be obtained by screening large numbers of mutants for the increased activity as evidenced by an increase in B6 vitamer production as described in Example 4, or by selecting for mutants that are resistant to inhibitors that are specific for the PLP biosynthetic pathway, and screening among those mutants for an increase in B6 vitamer production. Examples of such inhibitors are isoniazid, iproniazid, and

10 ginkgotoxin (4'-methoxy pyridoxine) (Dempsey and Arcement (1971) J. Bacteriol. 107(2): 580-582; Pflug, W., and Lingens, F., (1978) Hoppe-Seyler's Z. Physiol. Chem. 359: 559-570; Fiehe, K., et al., (2000) J. Nat. Prod. 63(2): 185-189).

15 **EXAMPLE 8: Processing of biosynthetic B6 vitamers.**

A B6 vitamer produced by a genetically modified organism of the invention can be harvested and processed into a format that is appropriate for commercial use. For example, after culturing a B6 vitamer producing micro-organism in liquid culture, the entire culture, including cells can be dried by evaporation or by spray drying, and the resulting powder can be mixed into animal feeds. Alternatively, the cells can be first removed by centrifugation or filtration, and the resulting supernatant solution can be dried as described above. As another alternative, the B6 vitamer can be purified from the culture broth by techniques well known in the art, such as filtration, reverse osmosis, column chromatography (ion exchange, hydrophobic or hydrophilic adsorption, gel filtration, etc.), solvent extraction, precipitation, distillation, evaporation, and the like. If the B6 vitamer producing organism is a plant, then the appropriate portion of the plant (for example the leaves, stems, roots, flowers, fruits, seeds, or any combination thereof) can be harvested and processed. For example the plant material can be dried and used directly, or the material can be pulverized or ground and the B6 vitamer extracted and/or processed as described above for cultures.

The production organism can be a micro-organism that normally inhabits the gut of humans or an animal if interest (for example one of many bacteria of the genus *Lactobacillus*, such as *L. acidophilus*), and the B6 vitamer can be delivered by ingestion of the organism.

Equivalents

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the
5 following claims.

G O D C E P T I O N
C O M P A N Y

What is claimed:

1. An organism that has been genetically modified to comprise a recombinant DNA molecule that results in the increase of the activity of one or more enzymes that catalyze(s) a step in the biosynthesis of a B6 vitamer, such that B6 vitamer production from said modified organism is increased compared to B6 production in an unmodified parent organism.
2. The organism of claim 1, wherein B6 vitamer production is at least ten-fold higher than from the unmodified parent organism.
3. The organism of claim 1, wherein said enzyme is one or more of YaaD or YaaE.
4. The organism of claim 1, wherein said organism is genetically modified to overexpress one or more genes that encodes an enzyme that catalyzes a step in the biosynthesis of a B6 vitamer.
5. The organism of claim 4, wherein said genes are derived from *Bacillus*.
6. The organism of claim 4, wherein said genes are derived from *Bacillus subtilis*.
7. The organism of claim 4, wherein at least one of said genes is a *yaaD* gene.
8. The organism of claim 4, wherein at least one of said genes is a *yaaE* gene.
9. The organism of claim 4, wherein at least two of said genes are *yaaD* and *yaaE* genes.
10. The organism of claim 4, wherein said organism is a *Bacillus* strain.

11. The organism of claim 4, wherein said organism is *Bacillus subtilis*.
12. The organism of any one of claims 1-11, wherein said organism is 5 grown in a liquid culture and the total B6 vitamer concentration in the culture supernatant is at least 7.0 mg/liter.
13. A method of producing a B6 vitamer comprising culturing a microorganism that has been genetically modified to overexpress one or more genes that 10 encodes an enzyme that catalyzes a step in the biosynthesis of a B6 vitamer, such that B6 vitamer production from said modified organism is increased compared to B6 production in an unmodified parent organism, under conditions such that the B6 vitamer is produced.
14. The method of claim 13, wherein said enzyme is one or more of YaaD or YaaE. 15
15. The method of claim 13, wherein at least one of said genes is a *yaaD* gene. 20
16. The method of claim 13, wherein at least one of said genes is a *yaaE* gene.
17. The method of claim 13, wherein said genes are contained on the 25 *yaaDE* operon.
18. The method of claim 13, wherein the B6 vitamer is pyridoxine.
19. The method of claim 13, wherein the B6 vitamer is pyridoxal. 30
20. The method of claim 13, wherein the B6 vitamer is pyridoxamine.
21. The method of claim 13, wherein the said genes are bacterial-derived. 35
22. The method of claim 13, wherein said genes are derived from *Bacillus*.

23. The method of claim 13, wherein said genes are derived from *Bacillus subtilis*.

5 24. The method of claim 13, wherein the microorganism is Gram positive.

10 25. The method of claim 13, wherein the microorganism is a microorganism belonging to a genus selected from the group consisting of *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*.

20 26. The method of claim 13, wherein the microorganism is of the genus *Bacillus*.

15 27. The method of claim 13, wherein the microorganism is *Bacillus subtilis*.

20 28. The method of claim 13, further comprising recovering the B6 vitamer.

25 29. A method of producing a B6 vitamer comprising culturing a microorganism that overexpresses at least one *Bacillus* B6 vitamer biosynthetic gene under conditions such that the B6 vitamer is produced.

30 30. The method of claim 29, wherein the microorganism overexpresses at least one *Bacillus subtilis* B6 vitamer biosynthetic enzyme.

35 31. The method of claim 29, wherein the B6 vitamer is pyridoxine.

30 32. The method of claim 29, wherein the B6 vitamer is pyridoxal.

33. The method of claim 29, wherein the B6 vitamer is pyridoxamine.

34. The method of claim 29, wherein the microorganism overexpresses at least two B6 vitamer biosynthetic enzymes.

35. The method of claim 29, wherein the microorganism is Gram positive.

36. The method of claim 29, wherein the microorganism is Gram negative.

37. The method of claim 29, wherein the microorganism is a microorganism belonging to a genus selected from the group consisting of *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*.

10 38. The method of claim 29, wherein the microorganism is of the genus *Bacillus*.

15 39. The method of claim 29, wherein the microorganism is *Bacillus subtilis*.

20 40. The method of claim 29, further comprising recovering the B6 vitamer.

25 41. A recombinant microorganism that overexpresses at least one *Bacillus* B6 vitamer biosynthetic gene.

42. A recombinant microorganism that overexpresses at least one *Bacillus* B6 vitamer biosynthetic enzyme.

25 43. The method of claim 42, wherein said enzyme is YaaD or YaaE.

44. The recombinant microorganism of claim 41 that overexpresses at least one *Bacillus subtilis* B6 vitamer biosynthetic gene.

30 45. The recombinant microorganism of claim 41, wherein the B6 vitamer biosynthetic gene is selected from the group consisting of *yaaD* and *yaaE*.

35 46. The recombinant microorganism of claim 41, that is Gram positive.

47. The recombinant microorganism of claim 41 belonging to a genus selected from the group consisting of *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*.

5 48. The recombinant microorganism of claim 41 belonging to the genus *Bacillus*.

10 49. The recombinant microorganism of claim 41 which is *Bacillus subtilis*.

15 50. A recombinant microorganism selected from the group consisting of PX14 and PX17.

20 51. A vector comprising a nucleic acid sequence that encodes at least one *Bacillus* B6 vitamer biosynthetic gene operably linked to regulatory sequences.

25 52. The vector of claim 51, comprising a nucleic acid sequence that encodes at least one *Bacillus subtilis* B6 vitamer biosynthetic gene.

30 53. The vector of claim 51, wherein the regulatory sequences comprise a constitutively active promoter.

54. The vector of claim 51, wherein the constitutively active promoter comprises P_{15} (SEQ ID NO:9) or P_{26} (SEQ ID NO:10) sequences.

35 55. The vector of claim 51, wherein the regulatory sequences comprise at least one artificial ribosome binding site (RBS).

56. A vector selected from the group consisting of pDX14R and pDX17R.

57. A recombinant microorganism comprising the vector of claim 56.

35 58. An isolated nucleic acid molecule that encodes at least one *Bacillus* B6 vitamer biosynthetic gene.

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59. The isolated nucleic acid molecule of claim 58 that encodes at least one *Bacillus subtilis* B6 vitamer biosynthetic gene.

60. An isolated *Bacillus* B6 vitamer biosynthetic enzyme polypeptide.

61. An isolated *Bacillus subtilis* B6 vitamer biosynthetic enzyme polypeptide.

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**METHODS AND ORGANISMS FOR
PRODUCTION OF B6 VITAMERS**

5 Abstract of the Disclosure

The present invention features methods of producing B6 vitamers that involve culturing an organism overexpressing an enzyme that catalyzes a step in the biosynthesis of a B6 vitamer under conditions such that a B6 vitamer is produced. The 10 present invention further features methods of producing B6 vitamers that involve culturing recombinant microorganisms that overexpress at least one B6 vitamer biosynthetic gene, e.g., *yaaD* or *yaaE*.

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Figure 1

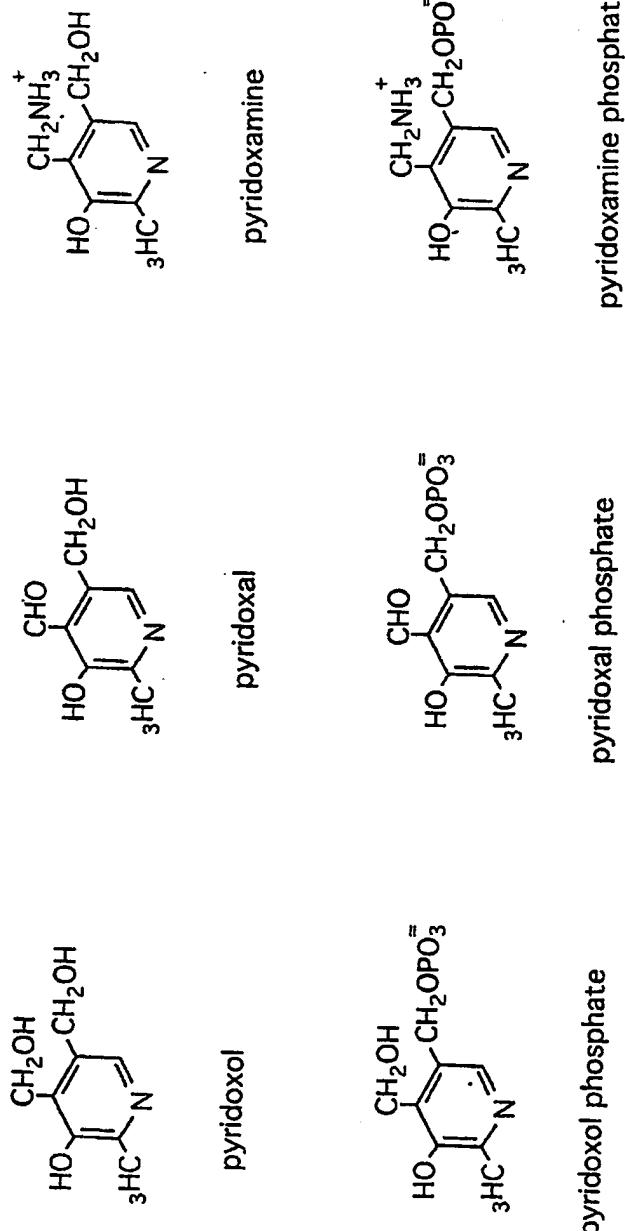


Figure 2

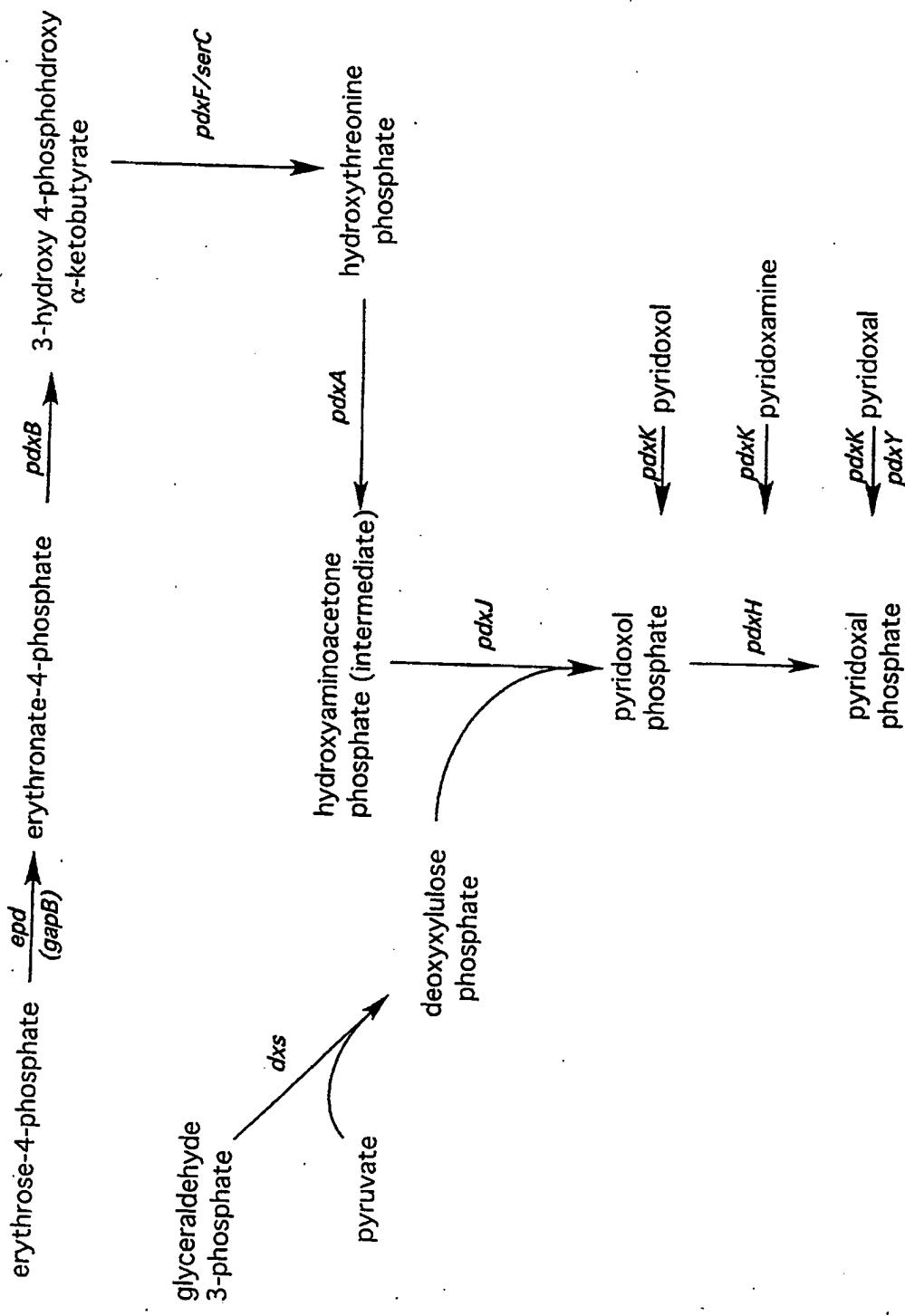


Figure 3

Effect of Vitamer Concentration on OD₆₀₀

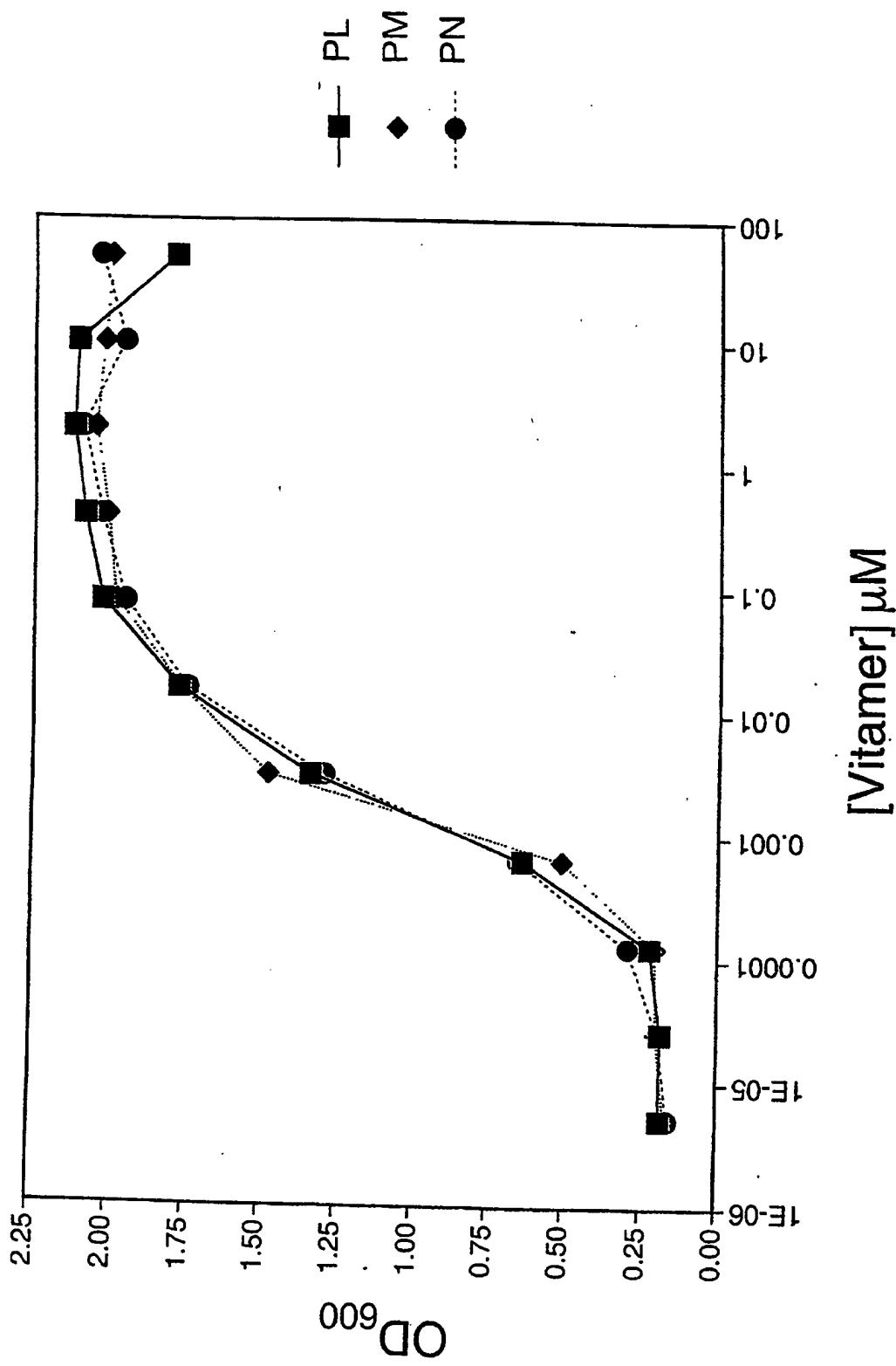


Figure 4. Structure of pDX1F

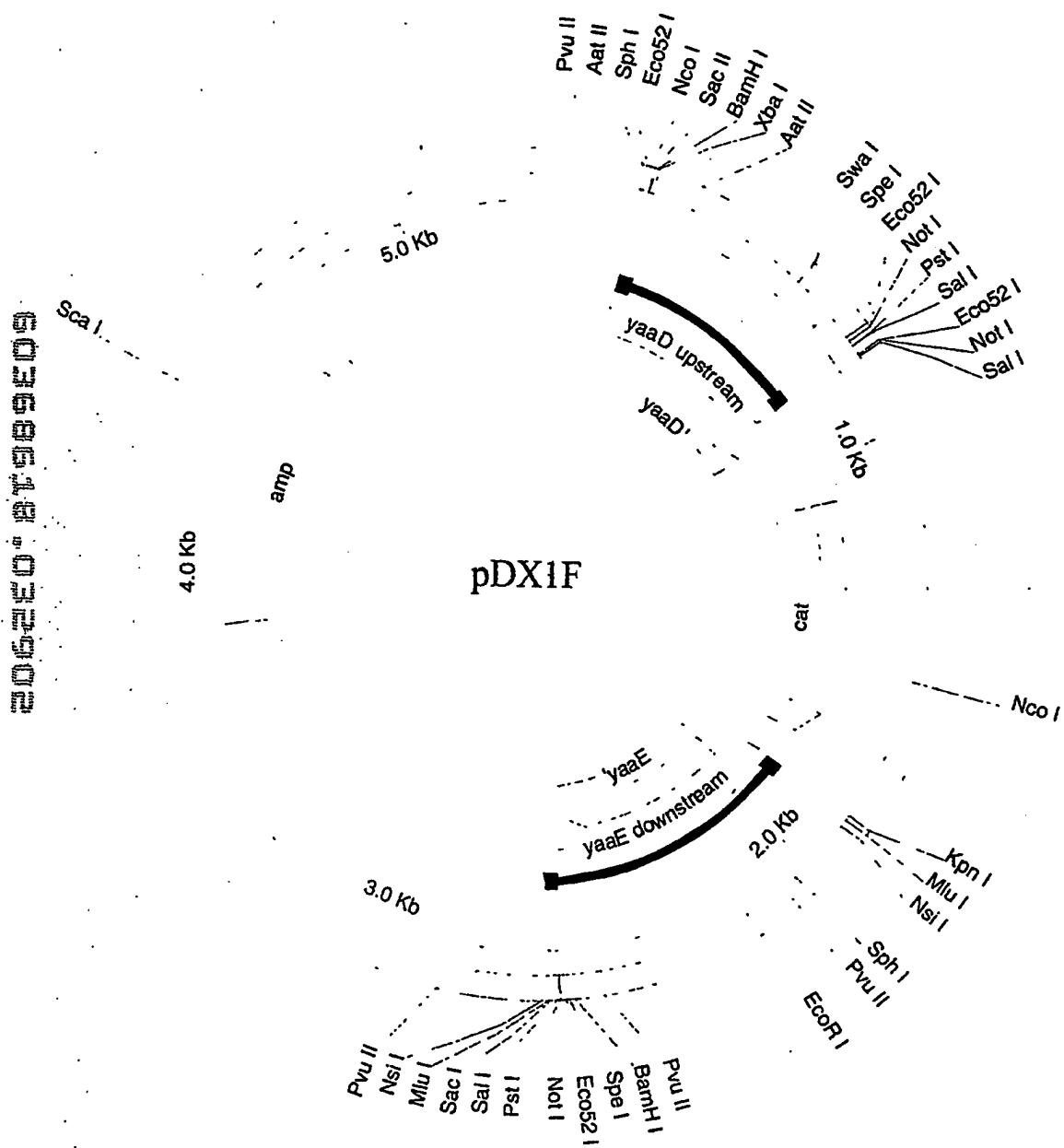


Figure 5. Structure of pDX11F

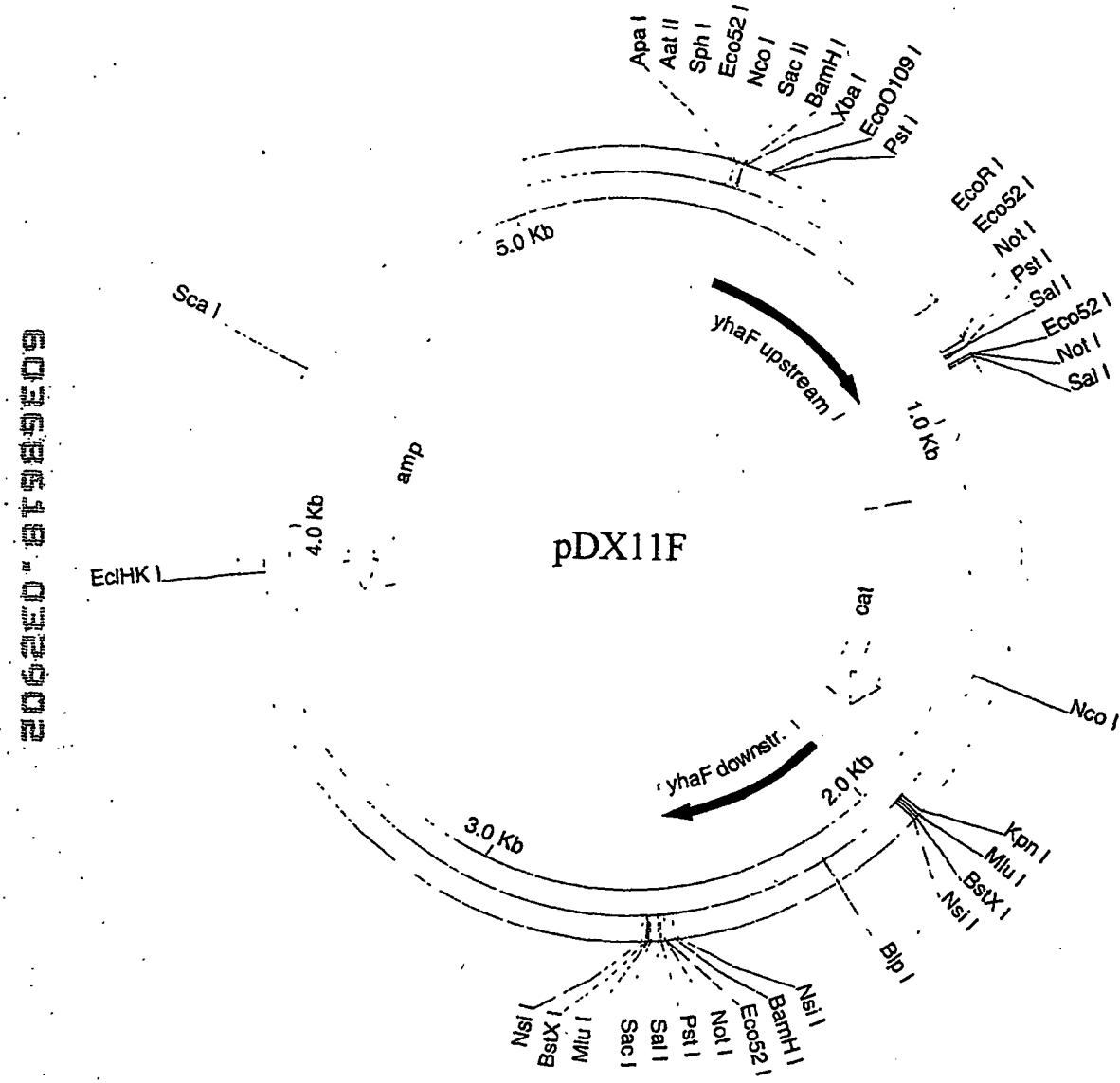


Figure 6

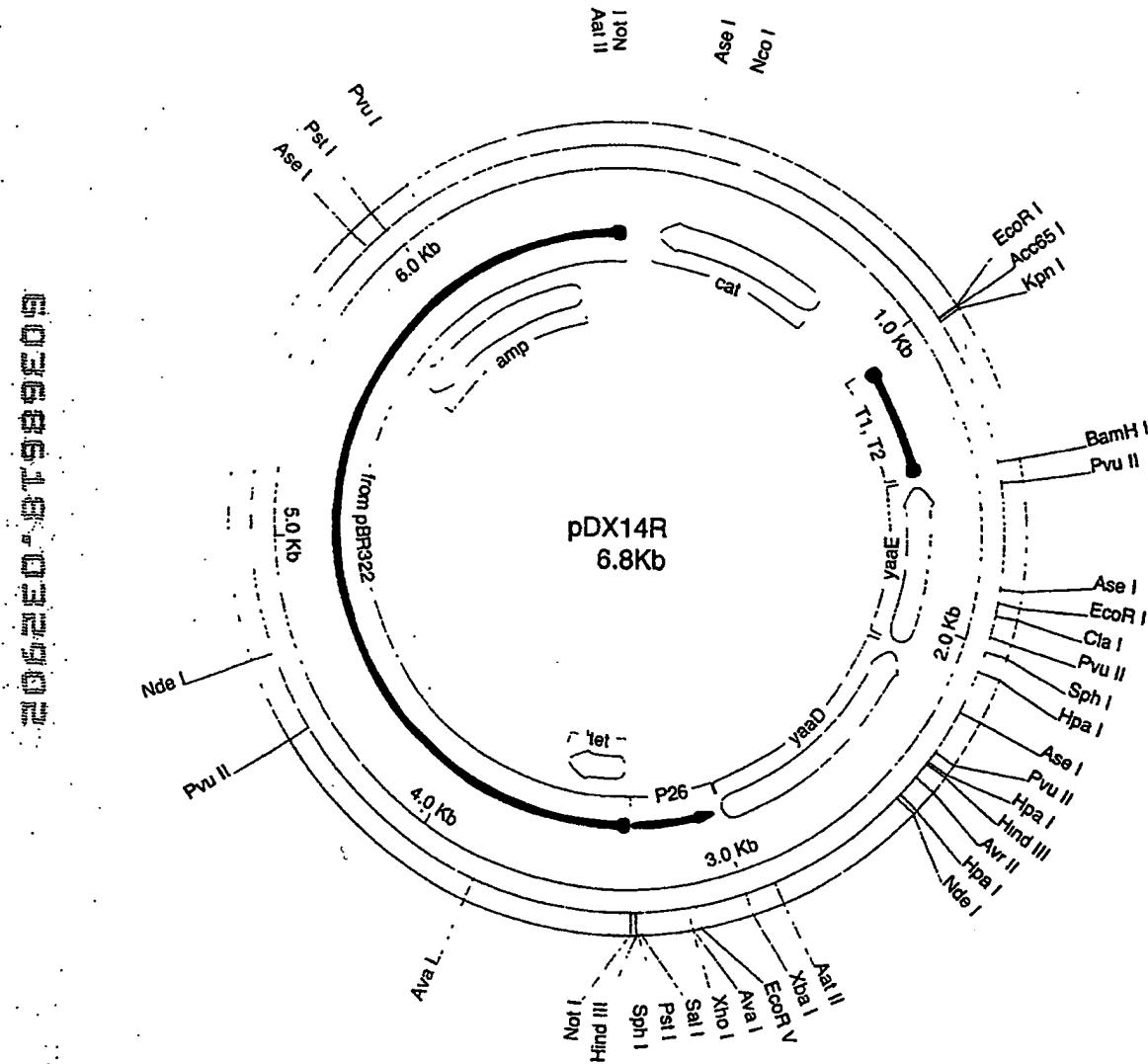
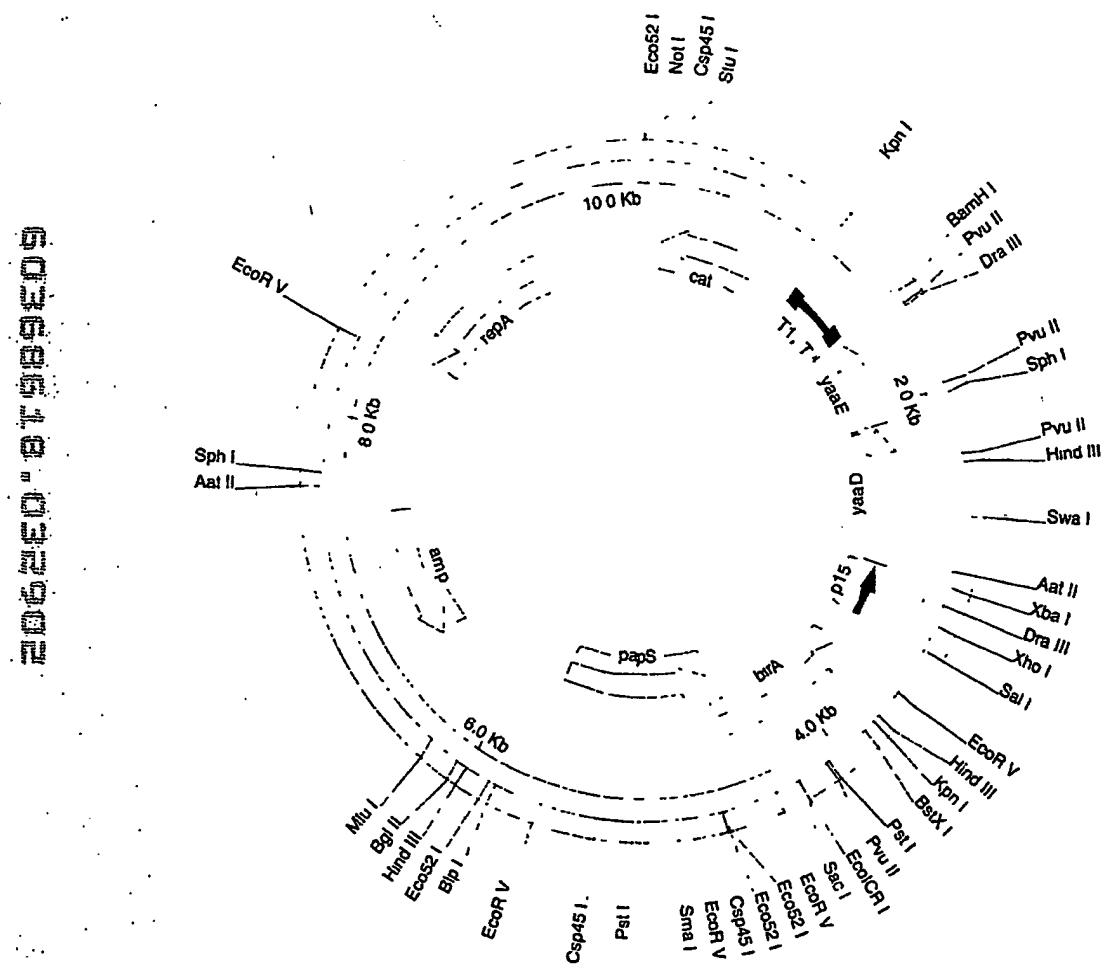


FIGURE 7. Structure of *pDX17R*



SEQUENCE LISTING

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Williams, Mark K.
Pero, Janice G.

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<213> Artificial Sequence

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All Databases



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EMBOSS Transeq

Transeq translates nucleic acid sequences to the corresponding peptide sequence. It can translate 3 forward or three reverse sense frames, or in all three forward or reverse frames, or in all six frames.

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Enter or Paste a nucleic acid Sequence in any format:

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EMBL-EBI

000

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EMBOSS Transeq Results

Transeq Results

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Regions	START-END
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ARG*
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BLAST Basic Local Alignment Search Tool

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Protein Sequence (243 letters)

Results for: Icl|79748 None(243aa)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

Icl|79748

Description

None

Molecule type

amino acid

Query Length

243

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

ProgramBLASTP 2.2.19+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#) [\[Related Structures\]](#)

Search Parameters

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Hitlist size	100
Gapcosts	11,1
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Composition-based stats	2
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Database

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Number of sequences	7,788,834

Entrez query none

Karlin-Altschul statistics

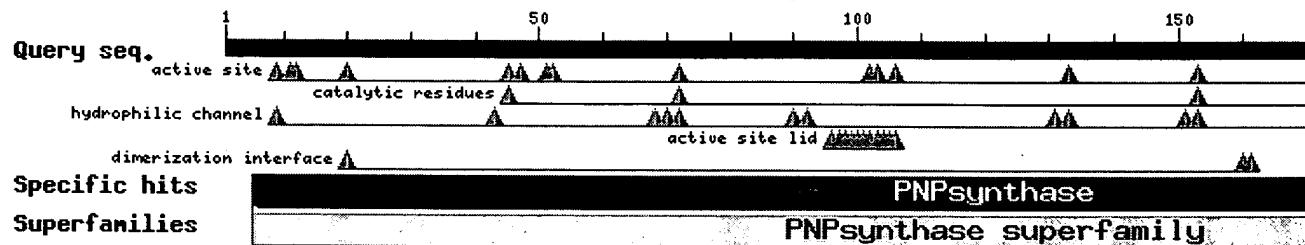
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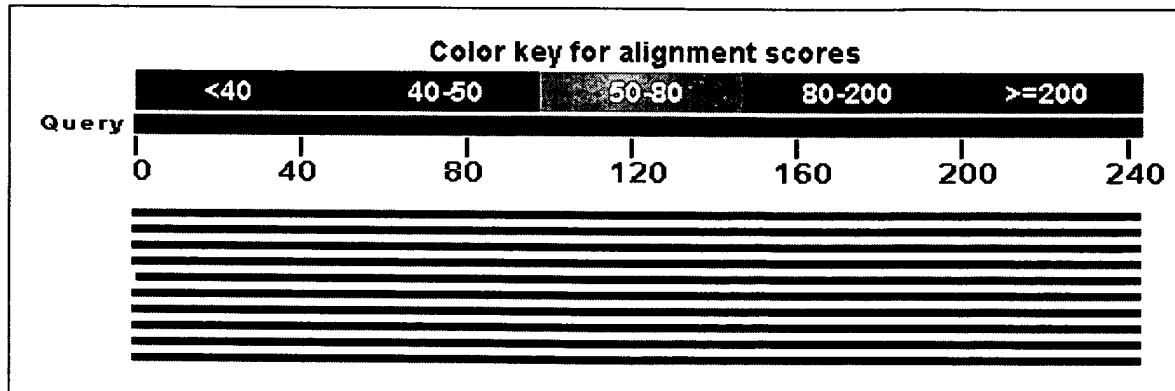
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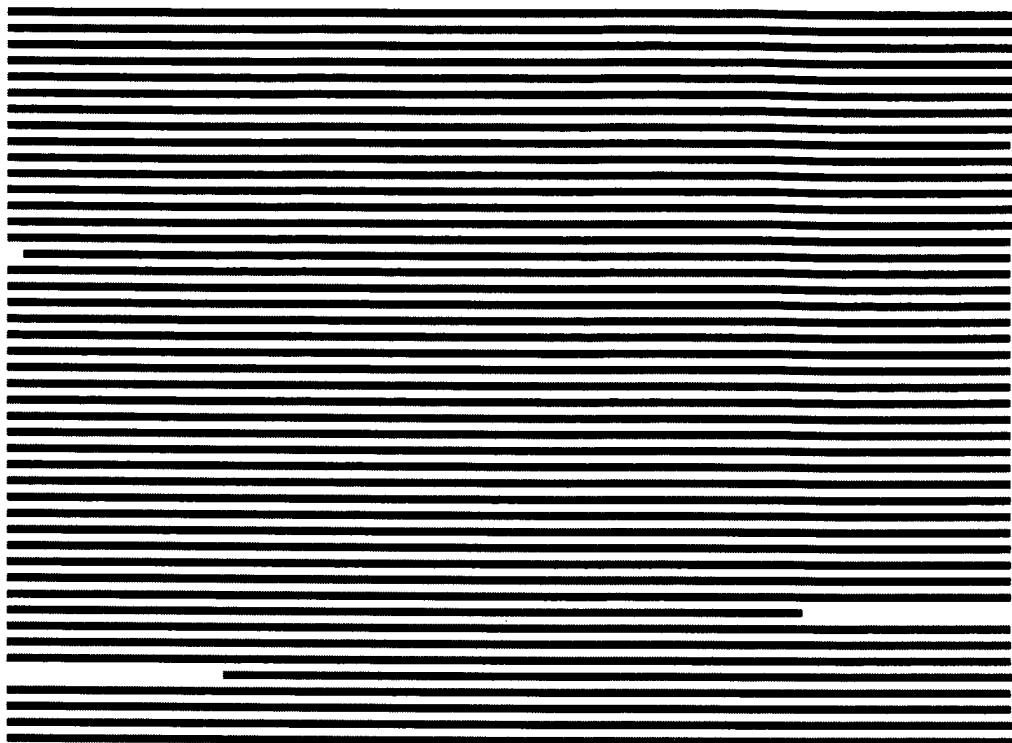
Graphic SummaryShow Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.

**Distribution of 100 Blast Hits on the Query Sequence**

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





The sequence information has been redacted by a large rectangular area filled with horizontal black bars.

[Descriptions](#)

		Score
E	Sequences producing significant alignments:	(Bits) Value
<u>ref NP_311457.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	491 3e-137
<u>ref YP_002330339.1 </u>	pyridoxine 5'-phosphate synthase [Escherichia...	489 6e-137
<u>ref NP_289121.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	489 1e-136
<u>ref YP_404339.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	488 1e-136
<u>pdb 1HO1 A</u>	Chain A, Crystal Structure Of Pyridoxine 5'-Phosphate ...	488 1e-136
<u>ref YP_001744753.1 </u>	pyridoxine 5'-phosphate synthase [Escherichia...	483 2e-136
<u>ref YP_403963.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	486 6e-136
<u>ref NP_838137.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	486 6e-136
<u>ref YP_311545.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	486 9e-136
<u>ref ZP_02902009.1 </u>	pyridoxine 5'-phosphate synthase [Escherichia...	485 1e-135
<u>ref YP_541876.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	484 3e-135
<u>gb ABK20147.1 </u>	pyridoxal phosphate biosynthetic protein [Shigella...	483 4e-135
<u>ref YP_670456.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	483 5e-135
<u>ref NP_754969.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	482 1e-134
<u>sp Q8FF18.3 PDXJ ECOL6</u>	RecName: Full=Pyridoxine 5'-phosphate ...	482 1e-134
<u>ref YP_001451819.1 </u>	pyridoxal phosphate biosynthetic protein ...	480 5e-134
<u>ref YP_001336529.1 </u>	pyridoxal phosphate biosynthetic protein ...	462 1e-128
<u>ref YP_002237093.1 </u>	pyridoxine 5'-phosphate synthase [Klebsiella...	462 1e-128
<u>ref ZP_03263636.1 </u>	hypothetical protein ENTCAN_03445 [Enterobacter...	461 2e-128
<u>ref NP_457107.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	461 3e-128
<u>ref NP_461513.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	460 4e-128
<u>ref YP_149621.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	460 4e-128
<u>ref YP_001569382.1 </u>	pyridoxal phosphate biosynthetic protein ...	459 1e-127
<u>ref YP_002147536.1 </u>	pyridoxine 5'-phosphate synthase [Salmonella...	458 2e-127
<u>ref YP_001177766.1 </u>	pyridoxal phosphate biosynthetic protein ...	451 3e-125
<u>ref ZP_03086581.1 </u>	pyridoxal phosphate biosynthetic protein P...	451 3e-125
<u>ref YP_001436809.1 </u>	pyridoxal phosphate biosynthetic protein ...	437 3e-121
<u>ref ZP_00822617.1 </u>	COG0854: Pyridoxal phosphate biosynthesis ...	397 4e-109
<u>ref ZP_00830259.1 </u>	COG0854: Pyridoxal phosphate biosynthesis ...	394 3e-108
<u>ref YP_001005353.1 </u>	pyridoxal phosphate biosynthetic protein ...	393 5e-108
<u>ref YP_001400120.1 </u>	pyridoxal phosphate biosynthetic protein ...	392 2e-107
<u>ref NP_663623.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	391 2e-107
<u>pdb 3F4N A</u>	Chain A, Crystal Structure Of Pyridoxal Phosphate ...	391 3e-107
<u>ref ZP_00833834.1 </u>	COG0854: Pyridoxal phosphate biosynthesis ...	390 4e-107
<u>ref ZP_00827187.1 </u>	COG0854: Pyridoxal phosphate biosynthesis ...	390 4e-107
<u>ref YP_071394.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	390 4e-107
<u>ref YP_051364.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	390 7e-107
<u>ref YP_001479390.1 </u>	pyridoxal phosphate biosynthetic protein ...	382 1e-104
<u>ref YP_455464.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	381 3e-104
<u>ref NP_930557.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	376 7e-103
<u>ref YP_855346.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	376 9e-103
<u>ref ZP_03318787.1 </u>	hypothetical protein PROVALCAL_01725 [Providencia...	373 7e-102
<u>ref ZP_02961267.1 </u>	hypothetical protein PROSTU_03281 [Providencia...	373 7e-102
<u>ref YP_002151612.1 </u>	pyridoxal phosphate biosynthetic protein ...	372 1e-101
<u>ref YP_001143199.1 </u>	pyridoxal phosphate biosynthetic protein ...	372 2e-101
<u>ref ZP_03315319.1 </u>	hypothetical protein PROVRUST_02121 [Providencia...	367 4e-100

<u>ref ZP_01262022.1 </u>	pyridoxal phosphate biosynthetic protein [...]	361	3e-98
<u>ref ZP_03385196.1 </u>	pyridoxal phosphate biosynthetic protein P...	360	4e-98
<u>ref YP_205467.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	360	5e-98
<u>ref YP_002073491.1 </u>	pyridoxal phosphate biosynthetic protein ...	358	1e-97
<u>ref YP_002156883.1 </u>	pyridoxal phosphate biosynthetic protein ...	358	2e-97
<u>ref ZP_03400922.1 </u>	pyridoxal phosphate biosynthetic protein P...	357	5e-97
<u>ref NP_760465.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	356	9e-97
<u>ref YP_131204.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	355	1e-96
<u>ref ZP_01816562.1 </u>	pyridoxal phosphate biosynthetic protein P...	354	3e-96
<u>ref YP_001906938.1 </u>	Pyridoxal phosphate biosynthetic protein ...	354	4e-96
<u>ref ZP_01161526.1 </u>	pyridoxal phosphate biosynthetic protein [...]	353	7e-96
<u>ref YP_002127690.1 </u>	pyridoxal phosphate biosynthetic protein ...	353	1e-95
<u>ref ZP_01870295.1 </u>	pyridoxal phosphate biosynthetic protein P...	352	1e-95
<u>ref YP_588729.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	352	1e-95
<u>ref ZP_01220096.1 </u>	pyridoxal phosphate biosynthetic protein [...]	352	2e-95
<u>ref YP_002263870.1 </u>	pyridoxal phosphate biosynthetic protein ...	352	2e-95
<u>ref ZP_01236135.1 </u>	pyridoxal phosphate biosynthetic protein [...]	352	2e-95
<u>gb EED26525.1 </u>	pyridoxal phosphate biosynthetic protein PdxJ ...	351	2e-95
<u>ref ZP_01988133.1 </u>	pyridoxal phosphate biosynthetic protein P...	350	4e-95
<u>ref ZP_01215567.1 </u>	pyridoxal phosphate biosynthetic protein [...]	350	5e-95
<u>ref ZP_01064680.1 </u>	pyridoxal phosphate biosynthetic protein [...]	349	1e-94
<u>gb EAZ49556.1 </u>	pyridoxal phosphate biosynthetic protein PdxJ ...	348	2e-94
<u>ref NP_798948.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	348	3e-94
<u>ref ZP_00991369.1 </u>	pyridoxal phosphate biosynthetic protein [...]	347	4e-94
<u>ref NP_232087.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	347	5e-94
<u>ref ZP_02196848.1 </u>	pyridoxal phosphate biosynthetic protein P...	347	6e-94
<u>ref ZP_01681976.1 </u>	pyridoxal phosphate biosynthetic protein P...	347	7e-94
<u>ref ZP_01949430.1 </u>	pyridoxal phosphate biosynthetic protein P...	345	1e-93
<u>ref YP_663265.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	345	2e-93
<u>ref ZP_03354955.1 </u>	pyridoxal phosphate biosynthetic protein P...	343	6e-93
<u>ref ZP_01898798.1 </u>	pyridoxal phosphate biosynthetic protein [...]	343	7e-93
<u>ref ZP_03347562.1 </u>	pyridoxal phosphate biosynthetic protein P...	340	6e-92
<u>ref ZP_01614216.1 </u>	pyridoxal phosphate biosynthetic protein [...]	339	1e-91
<u>ref ZP_01450587.1 </u>	pyridoxal phosphate biosynthetic protein [...]	338	3e-91
<u>ref YP_563765.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	335	1e-90
<u>ref YP_001553716.1 </u>	pyridoxal phosphate biosynthetic protein ...	335	2e-90
<u>ref YP_270774.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	335	2e-90
<u>ref YP_734973.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	335	3e-90
<u>ref YP_339261.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	334	4e-90
<u>ref YP_002359017.1 </u>	pyridoxal phosphate biosynthetic protein ...	334	4e-90
<u>ref YP_001365462.1 </u>	pyridoxal phosphate biosynthetic protein ...	334	4e-90
<u>ref YP_001182689.1 </u>	pyridoxal phosphate biosynthetic protein ...	333	8e-90
<u>ref YP_001049591.1 </u>	pyridoxal phosphate biosynthetic protein ...	333	8e-90
<u>ref YP_001500902.1 </u>	pyridoxal phosphate biosynthetic protein ...	332	1e-89
<u>ref YP_733968.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	332	2e-89
<u>ref YP_751604.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	332	2e-89
<u>ref YP_964373.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	332	2e-89
<u>ref YP_001673314.1 </u>	pyridoxal phosphate biosynthetic protein ...	330	7e-89
<u>ref YP_001093187.1 </u>	pyridoxal phosphate biosynthetic protein ...	329	1e-88
<u>ref YP_001759633.1 </u>	pyridoxal phosphate biosynthetic protein ...	329	1e-88
<u>ref YP_870654.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	329	1e-88
<u>ref NP_716971.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	328	2e-88
<u>ref YP_942095.1 </u>	pyridoxal phosphate biosynthetic protein Pdx...	328	3e-88

ref|YP_693348.1| pyridoxal phosphate biosynthetic protein Pdx... 328 3e-88

Alignments Select All Get selected sequences Distance tree of results

>ref|NP_311457.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia c O157:H7 str. Sakai]
ref|NP_417059.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli str. K-12 substr. MG1655]
ref|AP_003150.1| pyridoxine 5'-phosphate synthase [Escherichia coli str. K-12 substr. W3110]
 71 more sequence titles

ref|YP_001463887.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia E24377A]
ref|YP_001459361.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichi HS]
ref|ZP_02773388.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s EC4113]
ref|ZP_02782782.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s EC4401]
ref|ZP_02786192.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s EC4501]
ref|ZP_02793675.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s EC4486]
ref|ZP_02798517.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s EC4196]
ref|ZP_02803548.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s EC4076]
ref|ZP_02812931.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s EC869]
ref|ZP_02823953.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s EC508]
ref|YP_001724107.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichi ATCC 8739]
ref|YP_001731493.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli str. K DH10B]
ref|ZP_03002699.1| pyridoxal phosphate biosynthetic protein PdxJ [Escherichia c 53638]
ref|ZP_03029794.1| pyridoxine 5'-phosphate synthase [Escherichia coli B7A]
ref|ZP_03045127.1| pyridoxine 5'-phosphate synthase [Escherichia coli E22]
ref|ZP_03049293.1| pyridoxine 5'-phosphate synthase [Escherichia coli E110019]
ref|ZP_03061820.1| pyridoxine 5'-phosphate synthase [Escherichia coli B171]
ref|ZP_03069709.1| pyridoxine 5'-phosphate synthase [Escherichia coli 101-1]
ref|ZP_03082093.1| pyridoxal phosphate biosynthetic protein PdxJ [Escherichia c O157:H7 str. EC4024]
ref|ZP_03251256.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s EC4206]
ref|ZP_03255815.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s EC4045]
ref|ZP_03259661.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s EC4042]
ref|YP_002272039.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli O157:H EC4115]
ref|YP_002294127.1| **G** pyridoxal phosphate biosynthetic protein [Escherichia col
ref|ZP_03442750.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s TW14588]
ref|YP_002381699.1| **G** pyridoxine 5'-phosphate synthase [Escherichia fergusonii 35469]
ref|YP_002388058.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli IAI1]
ref|YP_002403859.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli 55989]
 sp|P0A794.2|PDXJ_ECOLI RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
 sp|P0A795.2|PDXJ_ECO57 RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN

pdb|1M5W|A **S** Chain A, 1.96 Å Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
pdb|1M5W|B **S** Chain B, 1.96 Å Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate

pdb|1M5W|C S Chain C, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
pdb|1M5W|D S Chain D, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
pdb|1M5W|E S Chain E, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
pdb|1M5W|F S Chain F, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
pdb|1M5W|G S Chain G, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
pdb|1M5W|H S Chain H, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
gb|AAA24315.1| pdxJ
gb|AAA21845.1| pdxJ
gb|AAA79826.1| CG Site No. 416
gb|AAC75617.1| G pyridoxine 5'-phosphate synthase [Escherichia coli str. K-12 substr. MG1655]
dbj|BAB36853.1| G pyridoxine biosynthesis [Escherichia coli O157:H7 str. Sakai]
dbj|BAE76740.1| pyridoxine 5'-phosphate synthase [Escherichia coli str. K12 sub W3110]
gb|ABV06978.1| G pyridoxine 5'-phosphate synthase [Escherichia coli HS]
gb|ABV20635.1| G pyridoxine 5'-phosphate synthase [Escherichia coli E24377A]
gb|ACA76780.1| G pyridoxal phosphate biosynthetic protein PdxJ [Escherichia col ATCC 8739]
gb|ACB03715.1| G pyridoxine 5'-phosphate synthase [Escherichia coli str. K12 su DH10B]
gb|EDU34578.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4196]
gb|EDU55194.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4113]
gb|EDU65731.1| pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli 53638]
gb|EDU72247.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4076]
gb|EDU73719.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4401]
gb|EDU80638.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4486]
gb|EDU86799.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4501]
gb|EDU90661.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC869]
gb|EDU97102.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC508]
gb|EDV61746.1| pyridoxine 5'-phosphate synthase [Escherichia coli B7A]
gb|EDV82886.1| pyridoxine 5'-phosphate synthase [Escherichia coli E22]
gb|EDV88722.1| pyridoxine 5'-phosphate synthase [Escherichia coli E110019]
gb|EDX28996.1| pyridoxine 5'-phosphate synthase [Escherichia coli B171]
gb|EDX39410.1| pyridoxine 5'-phosphate synthase [Escherichia coli 101-1]
gb|EDZ78321.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4206]
gb|EDZ84450.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4045]
gb|EDZ87146.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4042]
gb|ACI35060.1| G pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4115]
dbj|BAG78376.1| G pyridoxal phosphate biosynthetic protein [Escherichia coli SE]
gb|EEC27459.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. TW14588]
emb|CAU98723.1| G pyridoxine 5'-phosphate synthase [Escherichia coli]
emb|CAQ88058.1| G pyridoxine 5'-phosphate synthase [Escherichia fergusonii]
emb|CAQ99513.1| G pyridoxine 5'-phosphate synthase [Escherichia coli]

Length=243

GENE ID: 914900 ECs3430 | pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli O157:H7 str. Sakai] (Over 10 PubMed links)

Score = 491 bits (1263), Expect = 3e-137, Method: Compositional matrix adjust.
 Identities = 243/243 (100%), Positives = 243/243 (100%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTLTDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LRQTLTDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDAC	120
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Query 181	FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Query 241	ARG 243	
Sbjct 241	ARG 243	

>**ref|YP_002330339.1|** **G** pyridoxine 5'-phosphate synthase [Escherichia coli O127:H E2348/69]

ref|YP_002413587.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli UMN026

emb|CAS10389.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli O127:H6 st E2348/69]

emb|CAR14061.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli]
 Length=243

GENE ID: 7062394 **pdxJ** | pyridoxine 5'-phosphate synthase
 [Escherichia coli O127:H6 E2348/69] (10 or fewer PubMed links)

Score = 489 bits (1260), Expect = 6e-137, Method: Compositional matrix adjust.
 Identities = 242/243 (99%), Positives = 243/243 (100%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTLTDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LRQTLTDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDAC	120
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	KRLAEAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Query 181	FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Query 241	ARG 243	
Sbjct 241	ARG 243	

>**ref|NP_289121.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia c O157:H7 EDL933]

pir||C85902 pyridoxine biosynthesis [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

gb|AAG57679.1|AE005487_3 **G** pyridoxine biosynthesis [Escherichia coli O157:H7 ED Length=243]

GENE ID: 957924 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ
 [Escherichia coli O157:H7 EDL933] (10 or fewer PubMed links)

Score = 489 bits (1258), Expect = 1e-136, Method: Compositional matrix adjust.
 Identities = 242/243 (99%), Positives = 242/243 (99%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60

Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTEGGLDVAGQRDKMRDAC	120
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	KRLADAGIQVSLFIDADEEQIKAAAEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Query 181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Query 241	ARG 243	
Sbjct 241	ARG 243	

>[ref|YP_404339.1|](#) **G** pyridoxal phosphate biosynthetic protein PdxJ [Shigella dysenteriae Sd197]

sp|Q32CV7.1|PDXJ SHIDS G RecName: Full=Pyridoxine 5'-phosphate synthase; Short=
gb|ABB62848.1| G pyridoxine biosynthesis [Shigella dysenteriae Sd197]
Length=243

GENE ID: 3795506 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Shigella dysenteriae Sd197] (10 or fewer PubMed links)

Score = 488 bits (1257), Expect = 1e-136, Method: Compositional matrix adjust.
Identities = 242/243 (99%), Positives = 242/243 (99%), Gaps = 0/243 (0%)

Query 1	MAELLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTEGG DVAGQRDKMRDAC	120
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	KRLADAGIQVSLFIDADEEQIKAAAEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Query 181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Query 241	ARG 243	
Sbjct 241	ARG 243	

>[pdb|1HO1|A](#) **S** Chain A, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase
[pdb|1HO1|B](#) **S** Chain B, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase
[pdb|1HO1|C](#) **S** Chain C, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase
21 more sequence titles

[pdb|1HO1|D](#) **S** Chain D, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase
[pdb|1HO4|A](#) **S** Chain A, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With Pyridoxine 5'-Phosphate And Inorganic Phosphate
[pdb|1HO4|B](#) **S** Chain B, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With Pyridoxine 5'-Phosphate And Inorganic Phosphate
[pdb|1HO4|C](#) **S** Chain C, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With Pyridoxine 5'-Phosphate And Inorganic Phosphate
[pdb|1HO4|D](#) **S** Chain D, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With Pyridoxine 5'-Phosphate And Inorganic Phosphate
[pdb|1IXN|A](#) **S** Chain A, Enzyme-Substrate Complex Of Pyridoxine 5'-Phosphate Synthase
[pdb|1IXN|B](#) **S** Chain B, Enzyme-Substrate Complex Of Pyridoxine 5'-Phosphate Synthase
[pdb|1IXN|C](#) **S** Chain C, Enzyme-Substrate Complex Of Pyridoxine 5'-Phosphate

Synthase

pdb|1IXN|D **S** Chain D, Enzyme-Substrate Complex Of Pyridoxine 5'-Phosphate Synthase

pdb|1IXO|A **S** Chain A, Enzyme-Analogue Substrate Complex Of Pyridoxine 5'-Phosphate Synthase

pdb|1IXO|B **S** Chain B, Enzyme-Analogue Substrate Complex Of Pyridoxine 5'-Phosphate Synthase

pdb|1IXO|C **S** Chain C, Enzyme-Analogue Substrate Complex Of Pyridoxine 5'-Phosphate Synthase

pdb|1IXO|D **S** Chain D, Enzyme-Analogue Substrate Complex Of Pyridoxine 5'-Phosphate Synthase

pdb|1IXP|A **S** Chain A, Enzyme-Phosphate Complex Of Pyridoxine 5'-Phosphate Synthase

pdb|1IXP|B **S** Chain B, Enzyme-Phosphate Complex Of Pyridoxine 5'-Phosphate Synthase

pdb|1IXP|C **S** Chain C, Enzyme-Phosphate Complex Of Pyridoxine 5'-Phosphate Synthase

pdb|1IXP|D **S** Chain D, Enzyme-Phosphate Complex Of Pyridoxine 5'-Phosphate Synthase

pdb|1IXQ|A **S** Chain A, Enzyme-Phosphate2 Complex Of Pyridoxine 5'-Phosphate Synthase

pdb|1IXQ|B **S** Chain B, Enzyme-Phosphate2 Complex Of Pyridoxine 5'-Phosphate Synthase

pdb|1IXQ|C **S** Chain C, Enzyme-Phosphate2 Complex Of Pyridoxine 5'-Phosphate Synthase

pdb|1IXQ|D **S** Chain D, Enzyme-Phosphate2 Complex Of Pyridoxine 5'-Phosphate Synthase

Length=242

Score = 488 bits (1257), Expect = 1e-136, Method: Compositional matrix adjust.
Identities = 242/242 (100%), Positives = 242/242 (100%), Gaps = 0/242 (0%)

Query 2	AELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRL	61
Sbjct 1	AELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRL	60
Query 62	RQTLDTMNLMAVTEEMLAIAAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDACK	121
Sbjct 61	RQTLDTMNLMAVTEEMLAIAAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDACK	120
Query 122	RLADAGIQVSLFIDAEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIKAATF	181
Sbjct 121	RLADAGIQVSLFIDAEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIKAATF	180
Query 182	AASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLEA	241
Sbjct 181	AASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLEA	240
Query 242	RG 243	
Sbjct 241	RG 242	

>**ref|YP_001744753.1|** **G** pyridoxine 5'-phosphate synthase [Escherichia coli SMS-3-]
ref|YP_002408707.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli IAI39]
gb|ACB18311.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli SMS-3-5]
emb|CAR18891.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli]
Length=243

GENE ID: 6143419 **pdxJ** | pyridoxine 5'-phosphate synthase
[Escherichia coli SMS-3-5]

Score = 488 bits (1256), Expect = 2e-136, Method: Compositional matrix adjust.
Identities = 241/243 (99%), Positives = 243/243 (100%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60

Query	61	LRQTL DTRMN LEMAV TEEM LAIA VET KPH FCLV P EK R QEV TEG GLD VAG Q RD KMR DAC	120
Sbjct	61	LRQTL DTRMN LEMAV TEEM LAIA VET KPH FCLV P EK R QEV TEG GLD VAG Q R + KMR DAC	120
Query	121	KRLAD AGI QVSLF IDA DEEQ IKA AAAEV GAP FIE IHT GCY A DA KT DAE QAO ELARI AKA AT	180
Sbjct	121	KRLA+ AGI QVSLF IDA DEEQ IKA AAAEV GAP FIE IHT GCY A DA KT DAE QAO ELARI AKA AT	180
Query	181	FAASL GLKVNAGH GLT YHNV KAIA AI PEMHE LNIGH HAI I GRAV M TGLK DAVA EM KRLM LE	240
Sbjct	181	FAASL GLKVNAGH GLT YHNV KAIA AI PEMHE LNIGH HAI I GRAV M TGLK DAVA EM KRLM LE	240
Query	241	ARG 243	
Sbjct	241	ARG 243	

>[ref|YP_408963.1|](#) **G** pyridoxal phosphate biosynthetic protein PdxJ [Shigella boyd Sb227]

[ref|YP_001881343.1|](#) **G** pyridoxine 5'-phosphate synthase [Shigella boydii CDC 308]
[sp|Q31XS3.1|PDXJ SHIBS](#) RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
[gb|ABB67135.1|](#) **G** pyridoxine biosynthesis [Shigella boydii Sb227]
[gb|ACD10043.1|](#) **G** pyridoxine 5'-phosphate synthase [Shigella boydii CDC 3083-94]
Length=243

GENE ID: [3781575](#) **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ [Shigella boydii Sb227] (10 or fewer PubMed links)

Score = 486 bits (1252), Expect = 6e-136, Method: Compositional matrix adjust.
Identities = 240/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query	61	LRQTL DTRMN LEMAV TEEM LAIA VET KPH FCLV P EK R QEV TEG GLD VAG Q RD KMR DAC	120
Sbjct	61	LRQTL DTRMN LEMAV TEEM LAIA VET KPH FCLV P EK R QEV TEG GLD VAG Q R + KMR DAC	120
Query	121	KRLAD AGI QVSLF IDA DEEQ IKA AAAEV GAP FIE IHT GCY A DA KT DAE QAO ELARI AKA AT	180
Sbjct	121	KRL DAGI QVSLF IDA DEEQ IKA AAAEV GAP FIE IHT GCY A DA KT DAE QAO EL RIAKA AT	180
Query	181	FAASL GLKVNAGH GLT YHNV KAIA AI PEMHE LNIGH HAI I GRAV M TGLK DAVA EM KRLM LE	240
Sbjct	181	FAASL GLKVNAGH GLT YHNV KAIA AI PEMHE LNIGH HAI I GRAV M TGLK DAVA EM KRLM LE	240
Query	241	ARG 243	
Sbjct	241	ARG 243	

>[ref|NP_838137.1|](#) **G** pyridoxal phosphate biosynthetic protein PdxJ [Shigella flex 2a str. 2457T]

[ref|NP_708416.2|](#) **G** pyridoxal phosphate biosynthetic protein PdxJ [Shigella flex 2a str. 301]

[ref|YP_690029.1|](#) **G** pyridoxal phosphate biosynthetic protein PdxJ [Shigella flex 5 str. 8401]

[ref|ZP_03064347.1|](#) pyridoxine 5'-phosphate synthase [Shigella dysenteriae 1012]

[gb|AAP17947.1|](#) **G** pyridoxal phosphate biosynthetic protein [Shigella flexneri 2a str. 2457T]

[gb|AAN44123.2|](#) **G** pyridoxal phosphate biosynthetic protein [Shigella flexneri 2a str. 301]

[gb|ABF04724.1|](#) **G** pyridoxine biosynthesis [Shigella flexneri 5 str. 8401]

[gb|EDX35667.1|](#) pyridoxine 5'-phosphate synthase [Shigella dysenteriae 1012]
Length=243

GENE ID: [1079066](#) **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ [Shigella flexneri 2a str. 2457T] (10 or fewer PubMed links)

Score = 486 bits (1251), Expect = 6e-136, Method: Compositional matrix adjust.
Identities = 240/243 (98%), Positives = 242/243 (99%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTLTDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKQRQEVTEGGLDVAGQRDKMRDACP LRQTLTDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKQRQEVTEGGLDVAGQR+K+RDAC	120
Sbjct 61	LRQTLTDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKQRQEVTEGGLDVAGQRKIRDAC	120
Query 121	KRLADAGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
Sbjct 121	KRLADAGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQEL RIAKAAT	180
Query 181	FAASLGLKVNAGHGLTYHNVKIAAAIPMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	FAASLGLKVNAGHGLTYHNVKIAAAIPMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Query 241	ARG 243	
Sbjct 241	ARG 243	

>**ref|YP_311545.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Shigella sonnei Ss046]

sp|Q3YYV2.1|PDXJ SHISS G RecName: Full=Pyridoxine 5'-phosphate synthase; Short=
gb|AAZ89310.1| **G** pyridoxine biosynthesis [Shigella sonnei Ss046]
Length=243

GENE ID: 3669253 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Shigella sonnei Ss046] (10 or fewer PubMed links)

Score = 486 bits (1250), Expect = 9e-136, Method: Compositional matrix adjust.
Identities = 239/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTLTDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKQRQEVTEGGLDVAGQRDKMRDACP LRQTLTDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKQRQEVTEGGLDVAGQR+KMRDACP	120
Sbjct 61	LRQTLTDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKQRQEVTEGGLDVAGQRKIRDAC	120
Query 121	KRLADAGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
Sbjct 121	KRLTDAGIQISLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQEL RIAKAAT	180
Query 181	FAASLGLKVNAGHGLTYHNVKIAAAIPMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	FAASLGLKVNAGHGLTYHNVKIAAAIPMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Query 241	ARG 243	
Sbjct 241	ARG 243	

>**ref|ZP_02902009.1|** pyridoxine 5'-phosphate synthase [Escherichia albertii TW076]
gb|EDS92821.1| pyridoxine 5'-phosphate synthase [Escherichia albertii TW07627]
Length=243

Score = 485 bits (1249), Expect = 1e-135, Method: Compositional matrix adjust.
Identities = 240/243 (98%), Positives = 242/243 (99%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTLTDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKQRQEVTEGGLDVAGQRDKMRDACP LRQTLTDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKQRQEVTEGGLDVAGQR KMRDACP	120
Sbjct 61	LRQTLTDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKQRQEVTEGGLDVAGQRKIRDAC	120
Query 121	KRLADAGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
Sbjct 121	KRLADAGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAS	180
Query 181	FAASLGLKVNAGHGLTYHNVKIAAAIPMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	FAASLGLKVNAGHGLTYHNVKIAAAIPMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240

Query 241 ARG 243
 Sbjct 241 ARG 243

>**ref|YP_541876.1|** G pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli UTI89]
ref|YP_853698.1| G pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli APEC O1]
gb|ABE08345.1| G pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli UTI89]
gb|ABJ01984.1| G pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli APEC O1]
 Length=248

GENE ID: 3989796 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli UTI89] (10 or fewer PubMed links)

Score = 484 bits (1245), Expect = 3e-135, Method: Compositional matrix adjust.
 Identities = 240/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 6	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDV I	65
Query 61	LRQTLDTMRNLEMAMVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRD	120
Sbjct 66	LRQTLDTMRNLEMAMVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQR+KMRD	125
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 126	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	185
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLM	240
Sbjct 186	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLM	245
Query 241	ARG 243	
Sbjct 246	ARG 248	

>**gb|ABK20147.1|** pyridoxal phosphate biosynthetic protein [Shigella boydii]
 Length=243

Score = 483 bits (1244), Expect = 4e-135, Method: Compositional matrix adjust.
 Identities = 238/243 (97%), Positives = 239/243 (98%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADG TVHLREDRRHITDRDVRI	60
Query 61	LRQTLDTMRNLEMAMVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRD	120
Sbjct 61	LRQTLDTMRNLEMAMVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQR+KMRD	120
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQEL RIAKAAT	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLM	240
Sbjct 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKD VAEMKRLM	240
Query 241	ARG 243	
Sbjct 241	ARG 243	

>**ref|YP_670456.1|** G pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli 536]
ref|ZP_03035524.1| pyridoxine 5'-phosphate synthase [Escherichia coli F11]
ref|YP_002392398.1| G pyridoxine 5'-phosphate synthase [Escherichia coli S88]
 7 more sequence titles

ref|YP_002398892.1| G pyridoxine 5'-phosphate synthase [Escherichia coli ED1a]
ref|YP_002557403.1| G Pyridoxine 5'-phosphate synthase [Escherichia coli LF82]
gb|ABG70555.1| G pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli 536]
gb|EDV65320.1| pyridoxine 5'-phosphate synthase [Escherichia coli F11]
emb|CAR04001.1| G pyridoxine 5'-phosphate synthase [Escherichia coli]
emb|CAR09161.2| G pyridoxine 5'-phosphate synthase [Escherichia coli]
emb|CAP77010.1| G Pyridoxine 5'-phosphate synthase [Escherichia coli LF82]
Length=243

GENE ID: 4190772 ECP 2566 | pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli 536] (10 or fewer PubMed links)

Score = 483 bits (1244), Expect = 5e-135, Method: Compositional matrix adjust.
Identities = 240/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDV I	60
Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQR+KMRDAC	120
Query 121	KRLADAGIQVSLFIDADEEQIKAACAEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
Sbjct 121	KRLADAGIQVSLFIDADEEQIKAACAEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	FA SLGLKVNAHGHLTYHNVKAIAAIPMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Query 241	ARG 243	
Sbjct 241	ARG 243	

>**ref|NP_754969.1|** G pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli CFT073]

gb|AAN81537.1|AE016764_219 G Pyridoxal phosphate biosynthetic protein pdxJ [Escherichia coli CFT073]
Length=248

GENE ID: 1038793 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli CFT073] (10 or fewer PubMed links)

Score = 482 bits (1241), Expect = 1e-134, Method: Compositional matrix adjust.
Identities = 239/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 6	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDV I	65
Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDAC	120
Sbjct 66	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQR+KMRDAC	125
Query 121	KRLADAGIQVSLFIDADEEQIKAACAEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
Sbjct 126	KRLADAGIQVSLFIDADE+QIKAACAEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	185
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 186	FA SLGLKVNAHGHLTYHNVKAIAAIPMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	245
Query 241	ARG 243	
Sbjct 246	ARG 248	

>**sp|Q8FF18.3|PDXJ_ECOL6** RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
Length=243

Score = 482 bits (1240), Expect = 1e-134, Method: Compositional matrix adjust.
 Identities = 239/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDV I	60
Query 61	LRQTL DTRMN LEMAVTEEMLAI AVE T KPH FCCL VPEK R QEV T EGGL DVAG Q RD KMR DAC	120
Sbjct 61	LRQTL DTRMN LEMAVTEEMLAI AVE T KPH FCCL VPEK R QEV T EGGL DVAG Q RD KMR DAC + KMR DAC	120
Query 121	KRLADAGIQVSLFIDA DE EQI KAAA EVGAP FIEI HTGCYADAKTDAEQAQELARI AKA AT	180
Sbjct 121	KRLADAGIQVSLFIDA DE + QI KAAA EVGAP FIEI HTGCYADAKTDAEQAQELARI AKA AT	180
Query 181	FAASLGLKVNA GH GL TY HNV KAI AAI PEMHELNIGHAI I GRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	FA SLGLKVNA GH GL TY HNV KAI AAI PEMHELNIGHAI I GRAVMTGLKDAVAEMKRLMLE	240
Query 241	ARG 243	
Sbjct 241	ARG 243	

>**ref|YP_001451819.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Citrobacter ATCC BAA-895]

gb|ABV11383.1| **G** hypothetical protein CKO_00218 [Citrobacter koseri ATCC BAA-89 Length=243]

GENE ID: 5585068 CKO_00218 | pyridoxal phosphate biosynthetic protein PdxJ [Citrobacter koseri ATCC BAA-895]

Score = 480 bits (1235), Expect = 5e-134, Method: Compositional matrix adjust.
 Identities = 236/243 (97%), Positives = 242/243 (99%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTL DTRMN LEMAVTEEMLAI AVE T KPH FCCL VPEK R QEV T EGGL DVAG Q RD KMR DAC	120
Sbjct 61	LRQTL DTRMN LEMAVTEEMLAI AVE T KPH FCCL VPEK R QEV T EGGL DVAG Q RD KMR DAC	120
Query 121	KRLADAGIQVSLFIDA DE EQI KAAA EVGAP FIEI HTGCYADAKTDAEQAQELARI AKA AT	180
Sbjct 121	KRLADAGILVSLFIDA DE EQI KAAA ADVGAP YIEI HTGCYADAKTDAEQAQELARI AKA AT	180
Query 181	FAASLGLKVNA GH GL TY HNV KAI AAI PEMHELNIGHAI I GRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	FAASLGLKVNA GH GL TY HNV+ AIAA+ PEMHELNIGHAI I GRAVM+ GLK+ AVAEMKRLMLE	240
Query 241	ARG 243	
Sbjct 241	ARG 243	

>**ref|YP_001336529.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Klebsiella subsp. pneumoniae MGH 78578]

gb|ABR78299.1| **G** pyridoxal phosphate biosynthetic protein [Klebsiella pneumonia subsp. pneumoniae MGH 78578] Length=243

GENE ID: 5342763 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Klebsiella pneumoniae subsp. pneumoniae MGH 78578]

Score = 462 bits (1188), Expect = 1e-128, Method: Compositional matrix adjust.
 Identities = 228/243 (93%), Positives = 236/243 (97%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTL DTRMN LEMAVTEEMLAI AVE T KPH FCCL VPEK R QEV T EGGL DVAG Q RD KMR DAC	120
Sbjct 61	LRQTL HTRMN LEMAVTEEMLTIACETKPHFCCLVPEK R QEV T EGGL DVAG Q RD KMR DAC	120
Query 121	KRLADAGIQVSLFIDA DE EQI KAAA EVGAP FIEI HTGCYADAKTDAEQAQELARI AKA AT	180

Sbjct	121	+RLADAGI VSLFIDADE QIKAAA+VGAP+IEIHTGCYADAKTDAEQA+EL RIAKAAT QRLADAGILVSLFIDADEAQIKAAADVGA ^P YIEIHTGCYADAKTDAEQARELERIAKAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AASLGLKVNAGHGLTYHNVKAIAAA+PEMHELNIGHAIIGRAVM+GLK+AVAEMK LM L	240
Sbjct	181	YAASLGLKVNAGHGLTYHNVKAIAALPEMHELNIGHAIIGRAVMSGLKEAVAEMKCLMLE	240
Query	241	ARG 243	
Sbjct	241	ARG 243	

>**ref|YP_002237093.1|** **G** pyridoxine 5'-phosphate synthase [Klebsiella pneumoniae 3
gb|ACI11352.1| **G** pyridoxine 5'-phosphate synthase [Klebsiella pneumoniae 342]
Length=243

GENE ID: 6934996 pdxJ | pyridoxine 5'-phosphate synthase
[Klebsiella pneumoniae 342] (10 or fewer PubMed links)

Score = 462 bits (1188), Expect = 1e-128, Method: Compositional matrix adjust.
Identities = 227/243 (93%), Positives = 236/243 (97%), Gaps = 0/243 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query	61	LRQTL ^D TRMNLEMAVTEEMLAI ^A VETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC LR+ ^T L TRMNLEMAVTEEML IA ETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Sbjct	61	LRET ^L HTRMNLEMAVTEEMLTIACETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEGVAPFIEIHTGCYADAKTDAEQAQELARIKAAT +RLADAGI VSLFIDAD EQIKAAA+VGAP+IEIHTGCYADAKTDA QA+EL RIAKAAT	180
Sbjct	121	QRLADAGILVSLFIDADNEQIKAAADVGA ^P YIEIHTGCYADAKTDAGQAKELERIAKAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AASLGLKVNAGHGLTYHNVKAIAAA+PEMHELNIGHAIIGRAVM+GLK+AVAEMKRLMLE	240
Sbjct	181	YAASLGLKVNAGHGLTYHNVKAIAALPEMHELNIGHAIIGRAVMSGLKEAVAEMKRLMLE	240
Query	241	ARG 243	
Sbjct	241	ARG 243	

>**ref|ZP_03283638.1|** hypothetical protein ENTCAN_03445 [Enterobacter cancerogenus ATCC 35316]
gb|EEA13217.1| hypothetical protein ENTCAN_03445 [Enterobacter cancerogenus ATCC 35316]
Length=243

Score = 461 bits (1187), Expect = 2e-128, Method: Compositional matrix adjust.
Identities = 227/242 (93%), Positives = 235/242 (97%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query	61	LRQTL ^D TRMNLEMAVTEEMLAI ^A VETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC LRQTL ^D TRMNLEMAVTEEML AI A ETKPHFCCLVPEKRQEVTEGGLDVAGQ +KMRDAC	120
Sbjct	61	LRQTL ^D TRMNLEMAVTEEMLAIACETKPHFCCLVPEKRQEVTEGGLDVAGQPEKMRDAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEGVAPFIEIHTGCYADAKTDAEQAQELARIKAAT KRLADAGI VSLFIDAD+ QIKAAA+ GAP+IEIHTGCYADAK DAEQA+EL RIAKAAT	180
Sbjct	121	KRLADAGILVSLFIDADDAQIKAAADAGA ^P YIEIHTGCYADAKNDAEQAKELERIAKAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AASLGLKVNAGHGLTYHNVKAIAAA+PEMHELNIGHAIIGRAVM+GLKDAVAEMKRLMLE	240
Sbjct	181	YAASLGLKVNAGHGLTYHNVKAIAALPEMHELNIGHAIIGRAVMSGLKDAVAEMKRLMLE	240
Query	241	AR 242	
Sbjct	241	AR 242	

>**ref|NP_457107.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica serovar Typhi str. CT18]

ref|NP_804155.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica serovar Typhi str. Ty2]

ref|ZP_03358029.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica serovar Typhi str. E02-1180]
7 more sequence titles

ref|ZP_03364950.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica serovar Typhi str. E98-0664]

ref|ZP_03370878.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica serovar Typhi str. E98-2068]

ref|ZP_03376409.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica serovar Typhi str. J185]

sp|Q8Z4K6.2|PDXJ_SALTI RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN

pir|IAH0828 probable pyridoxal phosphate biosynthetic protein STY2824 [imported from Salmonella enterica subsp. enterica serovar Typhi (strain CT18)]

emb|CAD02780.1| **G** putative pyridoxal phosphate biosynthetic protein [Salmonella enterica subsp. enterica serovar Typhi]

gb|AA068004.1| **G** putative pyridoxal phosphate biosynthetic protein [Salmonella enterica subsp. enterica serovar Typhi Ty2]
Length=243

GENE ID: 1249133 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica subsp. enterica serovar Typhi str. CT18]
(10 or fewer PubMed links)

Score = 461 bits (1185), Expect = 3e-128, Method: Compositional matrix adjust.
Identities = 228/243 (93%), Positives = 234/243 (96%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGTYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTLDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LRQTL TRMNLEMAVTEEMLAIAVET+PHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Query 121	KRLADAGIQVSLFIDADEEQIKAACAEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT RLA AGIQVSLFIDADE QI AAAEVGAPFIEIHTGCY+A+TDAEQA+ELARIA AAT	180
Sbjct 121	ARLAAAGIQVSLFIDADERQINAACAEVGAPFIEIHTGCYANAETDAEQAKELARIASAAT	180
Query 181	FAASGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE AA LGLKVNAGHGLTYHNVKAIAA+PEMHELNIGHAIIGRAVMTGLK+AVAEMKRLMLE	240
Sbjct 181	LAARLGLKVNAGHGLTYHNVKAIAALPEMHELNIGHAIIGRAVMTGLKEAVAEMKRLMLE	240
Query 241	ARG 243	
Sbjct 241	ARG 243	

>ref|NP_461513.1| **G** putative pyridoxal phosphate biosynthetic protein PdxJ [Salmonella typhimurium LT2]
ref|ZP_02343149.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29]
ref|ZP_02573805.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701]
26 more sequence titles

ref|ZP_02663381.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. SL480]

ref|ZP_02668300.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL486]

ref|ZP_02683344.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Hadar str. RI_05P066]

ref|YP_002041841.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Newport str. SL254]

ref|YP_002046640.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL476]

ref|YP_002115641.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633]

ref|ZP_03165472.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA23]

ref|YP_002216645.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853]

ref|ZP_03220482.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Javiana str. GA_MM04042433]

ref|YP_002227475.1| G Pyridoxal phosphate biosynthetic protein pdxJ [Salmonella subsp. enterica serovar Gallinarum str. 287/91]

ref|YP_002244636.1| G Pyridoxal phosphate biosynthetic protein pdxJ [Salmonella subsp. enterica serovar Enteritidis str. P125109]

sp|Q8ZN19.2|PDXJ SALTY RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN

gb|AAL21472.1| G carries out condensation and ring closure step after PdxA in pyridoxine biosynthesis [Salmonella typhimurium LT2]

gb|ACF64860.1| G pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Newport str. SL254]

gb|ACF66310.1| G pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL476]

gb|ACF91091.1| G pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633]

gb|EDY26273.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA23]

gb|EDY28219.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. SL480]

gb|ACH75352.1| G pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853]

gb|EDZ06327.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Javiana str. GA_MM04042433]

emb|CAR38432.1| G Pyridoxal phosphate biosynthetic protein pdxJ [Salmonella ent subsp. enterica serovar Gallinarum str. 287/91]

gb|EDZ13051.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29]

gb|EDZ15860.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701]

gb|EDZ24330.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL486]

gb|EDZ36146.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Hadar str. RI_05P066]

emb|CAR34140.1| G Pyridoxal phosphate biosynthetic protein pdxJ [Salmonella ent subsp. enterica serovar Enteritidis str. P125109]
Length=243

GENE ID: 1254100 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Salmonella typhimurium LT2] (10 or fewer PubMed links)

Score = 460 bits (1184), Expect = 4e-128, Method: Compositional matrix adjust.
Identities = 228/243 (93%), Positives = 234/243 (96%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGT YPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LRQTL TRMNLEMAVTEEMLAIAVET+PHFCCLVPEKROEVTEGGLDVAGQRDKMRDAC	120
Query 121	KRLADAGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
Sbjct 121	RLA AGIQVSLFIDADE QI AAAEVGAPFIEIHTGCY+A+TDAEQA+ELARIA AAT	180
Query 181	FAASGLKLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	AA LGLKLKVNAHGHLTYHNVKAIAA+PEMHELNIGHAIIGRAVMTGLK+AVAEMKRLMLE	240
Query 241	ARG 243	
Sbjct 241	ARG 243	

>**ref|YP_149621.1|** G pyridoxal phosphate biosynthetic protein PdxJ [Salmonella en subsp. enterica serovar Paratyphi A str. ATCC 9150]

ref|YP_217560.1| G pyridoxal phosphate biosynthetic protein PdxJ [Salmonella en subsp. enterica serovar Choleraesuis str. SC-B67]

ref|YP_001586617.1| G pyridoxal phosphate biosynthetic protein PdxJ [Salmonella subsp. enterica serovar Paratyphi B str. SPB7]

17 more sequence titles

ref|ZP_02657214.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp.

enterica serovar Kentucky str. CDC 191]
ref|ZP_02700515.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Newport str. SL317]
ref|ZP_02833432.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Weltevreden str. HI N05-537]
ref|ZP_03075503.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Kentucky str. CVM29188]
ref|YP_002141117.1| **G** putative pyridoxal phosphate biosynthetic protein [Salmon enterica subsp. enterica serovar Paratyphi A str. AKU_12601]
ref|ZP_03214396.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Virchow str. SL491]
sp|Q57LD3.1|PDXJ SALCH RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
sp|Q3V7K1.1|PDXJ SALPA RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
gb|AAV76309.1| **G** putative pyridoxal phosphate biosynthetic protein [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
gb|AAX66479.1| **G** carries out condensation and ring closure step after PdxA in pyridoxine biosynthesis [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
gb|ABX65784.1| **G** hypothetical protein SPAB_00348 [Salmonella enterica subsp. en serovar Paratyphi B str. SPB7]
gb|EDX44722.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Kentucky str. CVM29188]
gb|EDX49461.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Newport str. SL317]
emb|CAR58387.1| **G** putative pyridoxal phosphate biosynthetic protein [Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601]
gb|EDZ03427.1| pyridoxine 5'-phosphate synthase [SaImonella enterica subsp. enterica serovar Virchow str. SL491]
gb|EDZ20478.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Kentucky str. CDC 191]
gb|EDZ28717.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Weltevreden str. HI_N05-537]
Length=243

GENE ID: 3178757 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] (10 or fewer PubMed links)

Score = 460 bits (1184), Expect = 4e-128, Method: Compositional matrix adjust. Identities = 228/243 (93%), Positives = 234/243 (96%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGT YPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEK RQEVTTEGGLDVAGQRDKMRD AC	120
Sbjct 61	LRQTL TRMNLEMAVTEEMLAIAVET+PHFCCLVPEK RQEVTTEGGLDVAGQRDKMRD AC	120
Query 121	KRLADAGIQVSLFIDA DEEQIKAAA EVGAPFIEIHTGCYADAKTDAEQAQELARI AKAAT RLA AGIQVSLFIDA DE QI AAAEVGAPFIEIHTGCY A+A+TDAEQA+ELARIA AAT	180
Sbjct 121	ARLAAAGIQVSLFIDA DEAQINAAA EVGAPFIEIHTGCYANAETDAEQAKELARIASAAT	180
Query 181	FAASGLKVNAGHGLTYHNVKIAAA PEMHELNIGHAI IGRAVMTGLKDAVAEMKRLMLE AA LGLKVNA GHGLTYHNVKIAAA PEMHELNIGHAI IGRAVMTGLK+AVAEMKRLMLE	240
Sbjct 181	LAARLGLKVNAGHGLTYHNVKIAA ALPEMHELNIGHAI IGRAVMTGLKEAVAEMKRLMLE	240
Query 241	ARG 243	
Sbjct 241	ARG 243	

>ref|YP_001569382.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella subsp. arizonae serovar 62:z4,z23:--]

gb|ABX20240.1| **G** hypothetical protein SARI_00300 [Salmonella enterica subsp. ar serovar 62:z4,z23:--]
Length=243

GENE ID: 5764319 SARI_00300 | pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica subsp. arizonae serovar 62:z4,z23:--]

Score = 459 bits (1180), Expect = 1e-127, Method: Compositional matrix adjust. Identities = 225/243 (92%), Positives = 233/243 (95%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
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Sbjct 1	MAELLLGVNIDHIATLRNARGT YPDPVQAAFIAEQAGADGITVHLREDRRHI+DRDVRI	60
Query 61	LRQTL DTRMNLEMAVTEEMLAIAAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LRQTL DTRMNLEMAVTEEMLAIAAVET+PHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Query 121	KRLADAGIQVSLFIDADEEQIKAQAAEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT RLA AGIQVSLFIDADE QI AAAEVGAPFIEIHTGCY+A+AKTDAEQA++ELARIA AAT	180
Sbjct 121	SRLAAAGIQVSLFIDADEAQINAAAEGAPFIEIHTGCYANAKTDAEQAQSKELARIASAAT	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE A LGLKVNAHGHLTYHNVKAIAA+PEMHELNIGHAIIGRAVM+GLK+AVAEMKRLMLE	240
Sbjct 181	LAVRLGLKVNAHGHLTYHNVKAIAALPEMHELNIGHAIIGRAVMSGLKEAVAEMKRLMLE	240
Query 241	ARG 243	
Sbjct 241	ARG 243	

>**ref|YP_002147536.1|** **G** pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Agona str. SL483]

gb|ACH50628.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Agona str. SL483]
Length=243

GENE ID: 6793014 pdxJ | pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Agona str. SL483]

Score = 458 bits (1179), Expect = 2e-127, Method: Compositional matrix adjust.
Identities = 227/243 (93%), Positives = 233/243 (95%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGT YPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTL DTRMNLEMAVTEEMLAIAAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LRQTL DTRMNLEMAVTEMLAIAAVET+PHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Query 121	KRLADAGIQVSLFIDADEEQIKAQAAEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT RLA AGIQVSLFIDADE QI AAAEVGAPFIEIHTGCY+A+AKTDAEQA+ELARIA AAT	180
Sbjct 121	ARLAAAGIQVSLFIDADERQINAAAEGAPFIEIHTGCYANAETDAEQAQELARIASAAT	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE AA LGLKVNAHGHLTYHNVKAIAA+PEMHELNIGHAIIGRAVMTGLK+AVAEMKRLMLE	240
Sbjct 181	LAARLGLKVNAHGHLTYHNVKAIAALPEMHELNIGHAIIGRAVMTGLKEAVAEMKRLMLE	240
Query 241	ARG 243	
Sbjct 241	ARG 243	

>**ref|YP_001177766.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Enterobacter sp. 638]

gb|ABP61715.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Enterobacter sp. 638]
Length=243

GENE ID: 5111760 Ent638_3051 | pyridoxal phosphate biosynthetic protein PdxJ [Enterobacter sp. 638]

Score = 451 bits (1160), Expect = 3e-125, Method: Compositional matrix adjust.
Identities = 222/242 (91%), Positives = 233/242 (96%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDV+I	60
Query 61	LRQTL DTRMNLEMAVTEEMLAIA ETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LRQTL DTRMNLEMAVTEEMLAIAACETKPHFCCLVPEKRQEVTEGGLDVAGQQDKMRDAC	120
Query 121	KRLADAGIQVSLFIDADEEQIKAQAAEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT KRLADAGI VSLFIDAD +QIKAAA VGAP+IEIHTGCYADA+ + QA+ELARIKAAT	180
Sbjct 121	KRLADAGILVSLFIDADFQIKAAAEGAPFIEIHTGCYADADEVQAQAKELARIKAAT	180

Query 181	FAASLGLKVNAGHGLTYHNVKAIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AASLGLKVNAGHGLTYHNVKAIA IPEM ELNIGHAIIGRAVM+GLK+AV+EMKRLMLE	240
Sbjct 181	YAASLGLKVNAGHGLTYHNVKAIAQIPEMFELNIGHAIIGRAVMSGLKEAVSEMKRLMLE	240
Query 241	AR 242	
Sbjct 241	AR 242	

>**ref|ZP_03086581.1|** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia c O157:H7 str. EC4024]
Length=239

Score = 451 bits (1159), Expect = 3e-125, Method: Compositional matrix adjust.
Identities = 220/238 (92%), Positives = 230/238 (96%), Gaps = 0/238 (0%)

Query 5	LLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRILRQT +LGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRILRQT	64
Sbjct 1	MLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRILRQT	60
Query 65	LDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDACKRLA LDTRMNLEMAVTEEML IA +TKPHFCCLVPEKRQEVTTEGGLDVAGQ DKMRDACKRLA	124
Sbjct 61	LDTRMNLEMAVTEEMLTACDTKPHFCCLVPEKRQEVTTEGGLDVAGQLDKMRDACKRLA	120
Query 125	DAGIQVSLFIDADEEQIKAAAEGVAPFIEIHTGCYADAKTDAEQAQELARIAKAATFAAS DAGI VSLFIDAD QIKAAA+VGAP+IEIHTGCYADAK DAEQA+EL RIAKAAT+AAS	184
Sbjct 121	DAGILVSLFIDADFAQIKAAAADVGVAPYIEIHTGCYADAKNDAEQAKELERIAKAATYAAS	180
Query 185	LGLKVNAGHGLTYHNVKAIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLEAR LGLKVNAGHGLTYHNVKAIAA+PEMHELNIGHAIIGRAVM+GLK+AV+EMKRLMLEAR	242
Sbjct 181	LGLKVNAGHGLTYHNVKAIAALPEMHELNIGHAIIGRAVMSGLKEAVSEMKRLMLEAR	238

>**ref|YP_001436809.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Enterobact ATCC BAA-894]

gb|ABU75973.1| **G** hypothetical protein ESA_00695 [Enterobacter sakazakii ATCC BA Length=243

GENE ID: 5551187 **ESA_00695** | pyridoxal phosphate biosynthetic protein PdxJ [Enterobacter sakazakii ATCC BAA-894]

Score = 437 bits (1124), Expect = 3e-121, Method: Compositional matrix adjust.
Identities = 216/242 (89%), Positives = 227/242 (93%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVR MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVR	60
Sbjct 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVR	60
Query 61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRD LRQTL TRMNLEMAVTEEML IA ETKPHFCCLVPEKRQEVTTEGGLDVAGQ DKMRD	120
Sbjct 61	LRQTLHTRMNLEMAVTEEMLTACETKPHFCCLVPEKRQEVTTEGGLDVAGQLDKMRD AC	120
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEGVAPFIEIHTGCYADAKTDAEQAQELARIAKAAT +RLA AGI VSLFIDAD QI AA VGAP+IEIHTGCYADA+ DA +A+EL RIAKAAT	180
Sbjct 121	QRLAAAGILVSLFIDADDNAQIDA AVAVGVAPYIEIHTGCYADAEDDATRARELERIAKAAT	180
Query 181	FAASLGLKVNAGHGLTYHNVKAIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AAS GLKVNAGHGLTYHNV+AIAA+PEMHELNIGHAIIGRAVM+GLK+AV+EMKRLMLE	240
Sbjct 181	YAASKGLKVNAGHGLTYHNVQ AIAALPEMHELNIGHAIIGRAVMSGLKEAVSEMKRLMLE	240
Query 241	AR 242	
Sbjct 241	AR 242	

>**ref|ZP_00822617.1|** COG0854: Pyridoxal phosphate biosynthesis protein [Yersinia ATCC 43970]
Length=243

Score = 397 bits (1020), Expect = 4e-109, Method: Compositional matrix adjust.
Identities = 198/242 (81%), Positives = 212/242 (87%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVR MA+LLLGVNIDHIATLRNARGT YPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVR	60
Sbjct 1	MADLLLGVNIDHIATLRNARGTIYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVR	60
Query 61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRD LRQT+ TRMNLEMAVT+EM+ IA E +PHFCCLVPEKRQEVTTEGGLDVAGQ DKM A	120

Sbjct	61	LRQTIQTRMNLEMAVTDEMVGIACELQPHFCCLVPEKRQEVTTEGGLDVAGQIDKMTVAV	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIKAAT RLA+AGI VSLFIDAD QI AA VGAP+IEIHTG YADA TD + EL RI KAAT	180
Sbjct	121	SRLAEAGILVSLFIDADMQRQIDAATVVGAPYIEIHTGAYADATTDLARQELVRITKAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AAS GLKVNAGHGLTYHNV+ IAA+PE+HELNIGHAIIG+AVMTGL AV+EMK LM E	240
Sbjct	181	YAASKGLKVNAGHGLTYHNVQPIAALPEIHELNIGHAIIGQAVMTGLAAAVSEMVKLMRE	240
Query	241	AR 242	
Sbjct	241	AR 242	

>**ref|ZP_00830259.1|** COG0854: Pyridoxal phosphate biosynthesis protein [Yersinia ATCC 33641]
Length=243

Score = 394 bits (1013), Expect = 3e-108, Method: Compositional matrix adjust.
Identities = 196/242 (80%), Positives = 211/242 (87%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI MA+LLLGVNIDHIATLRNARGT YPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MADLLLGVNIDHIATLRNARGTIYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query	61	LRQTLTDRMNLEMAVTTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDAC LRQT+ TRMNLEMAVT+EM+ IA E +PHFCCLVPEKRQEVTTEGGLDVAGQ DKM A	120
Sbjct	61	LRQTIQTRMNLEMAVTDEMVDIACELQPHFCCLVPEKRQEVTTEGGLDVAGQIDKMTIAV	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIKAAT RL+AGI VSLFIDAD QI AA VGAP+IEIHTG YADA +D + EL RIAKAAT	180
Sbjct	121	SRLSEAGILVSLFIDADMQRQIDAATVVGAPYIEIHTGAYADATSDLARQELVRIAKAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AA GLKVNAGHGLTYHNV+ IAA+PEMHELNIGHAIIG+AVM+GL AV EMK LM E	240
Sbjct	181	YAAGKGLKVNAGHGLTYHNVQPIAALPEMHELNIGHAIIGQAVMSGLATAVTEMVKLMRE	240
Query	241	AR 242	
Sbjct	241	AR 242	

>**ref|YP_001005353.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia e subsp. enterocolitica 8081]

emb|CAL11118.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia enter subsp. enterocolitica 8081]
Length=243

GENE ID: 4716617 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Yersinia enterocolitica subsp. enterocolitica 8081] (10 or fewer PubMed links)

Score = 393 bits (1010), Expect = 5e-108, Method: Compositional matrix adjust.
Identities = 196/242 (80%), Positives = 210/242 (86%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI MA+LLLGVNIDHIATLRNARGT YPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MADLLLGVNIDHIATLRNARGTIYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query	61	LRQTLTDRMNLEMAVTTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDAC LR+T+ TRMNLEMAVT+EM+ IA E +PHFCCLVPEKRQEVTTEGGLDVAGQ DKM A	120
Sbjct	61	LRETIQTRMNLEMAVTDEMVGIACEINPHFCCLVPEKRQEVTTEGGLDVAGQIDKMTVAV	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIKAAT RLA AGI VSLFIDAD QI AA VGAP+IEIHTG YADA +D + EL RIAKAAT	180
Sbjct	121	SRLAKAGILVSLFIDADMQRQIDAATVVGAPYIEIHTGAYADATSDLARQELVRIAKAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AAS GLKVNAGHGLTYHNV+ IAA+PEMHELNIGHAIIG+AVM+GL AV +MK LM E	240
Sbjct	181	YAASKGLKVNAGHGLTYHNVQPIAALPEMHELNIGHAIIGQAVMSGLAAAVTDMKVLRE	240
Query	241	AR 242	
Sbjct	241	AR 242	

>**ref|YP_001400120.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p

IP 31758]

gb|ABS47286.1| G pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseudo IP 31758]
Length=243

GENE ID: 5386119 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Yersinia pseudotuberculosis IP 31758] (10 or fewer PubMed links)

Score = 392 bits (1006), Expect = 2e-107, Method: Compositional matrix adjust.
Identities = 197/242 (81%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MA+LLLGVNIDHIATLRNARGT YPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDACP LRQT+ TRMNLEMAVT+EM+ IA + KPHFCCLVPEKRQEVTEGGLDVAGO DKM A	120
Sbjct 61	LRQTIQTRMNLEMAVTDEMVDIACDIKPHFCCLVPEKRQEVTEGGLDVAGQVDKMTLAV	120
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIKAAT RLAD GI VSLFIDAD QI AA GAP+IEIHTG YADA T E+ EL RIAKAAT	180
Sbjct 121	GRLADVGILVSLFIDADFRQIDAAVAAGAPYIEIHTGAYADASTVLERQAEMLRIAKAAT	180
Query 181	FAASGLKVNAGHGLTYHNVKAIAAIPMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AA GLKVNAGHGLTYHNV+ IAA+PEMHELNIGHAIIG+AVMTGL AV +MK LM E	240
Sbjct 181	YAAGKGLKVNAGHGLTYHNVQPIAALPEMHELNIGHAIIGQAVMTGLATAVTDMKVLRE	240
Query 241	AR 242	
Sbjct 241	AR	
	AR 242	

>**ref|NP_668623.1|** G pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest KIM]

ref|NP_993846.1| G pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest biovar Microtus str. 91001]

ref|YP_652279.1| G pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest Antiqua]
31 more sequence titles

ref|YP_647139.1| G pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pesti Nepal516]

ref|YP_001162910.1| G pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p Pestoides F]

ref|ZP_01887420.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest CA88-4125]

ref|YP_001607938.1| G pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p Angola]

ref|ZP_02224083.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest biovar Orientalis str. F1991016]

ref|ZP_02227818.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest biovar Orientalis str. IP275]

ref|ZP_02228990.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest biovar Antiqua str. E1979001]

ref|ZP_02238376.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest biovar Antiqua str. B42003004]

ref|ZP_02304312.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest biovar Antiqua str. UG05-0454]

ref|ZP_02313105.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest biovar Orientalis str. MG05-1020]

ref|ZP_02315362.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest biovar Mediaevalis str. K1973002]

ref|ZP_02332413.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest FV-1]

ref|YP_001719943.1| G pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p YPIII]

ref|YP_002347860.1| G pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p C092]

sp|Q8ZCP4.1|PDXJ_YERPE RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN

gb|AAM84874.1|AE013732_6 G pyridoxine biosynthesis [Yersinia pestis KIM]

gb|AAS62723.1| G pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Microtus str. 91001]

gb|ABG17539.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis Nepal1516]

gb|ABG14334.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis Antiqua]

emb|CAL21538.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pesti C092]

gb|ABP39937.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis Pestoides F]

gb|EDM41872.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis CA88-4125]

gb|ABX88699.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis Angola]

gb|EDR31495.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Orientalis str. IP275]

gb|EDR37091.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Orientalis str. F1991016]

gb|EDR44775.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Antiqua str. E1979001]

gb|EDR50752.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Antiqua str. B42003004]

gb|EDR56862.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Orientalis str. MG05-1020]

gb|EDR62700.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Antiqua str. UG05-0454]

gb|EDR67525.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Mediaevalis str. K1973002]

gb|ACA67490.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseudo YPIII]

Length=243

GENE ID: 1146247 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis KIM] (10 or fewer PubMed links)

Score = 391 bits (1005), Expect = 2e-107, Method: Compositional matrix adjust. Identities = 197/242 (81%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MA+LLLGVNIDHIATLRNARGT YPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTLDTRMNLEMAVTTEEMLAIAVETKPHFCCLVPEKRKQEVTEGGLDVAGQRDKMRDACP	120
Sbjct 61	LRQT+ TRMNLEMAVT+EM+ IA + KPHFCCLVPEKRKQEVTEGGLDVAGQ DKM A	120
Query 121	KRLADAGIQVSLFIDADEEQIKAQAAEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	RLAD GI VSIFIDAD QI AA GAP+IEIHTG YADA T E+ EL RIAKAAT	180
Query 181	GRLADVGILVSLFIDADFRQIDAAVAAGAPYIEIHTGAYADASTVLERQAELMRIAAT	180
Sbjct .181	FAASGLKLKVNAHGHLTYHNVKIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct .181	+AA GLKLVNAHGHLTYHNV+ IAA+PEMHELNIGHAIIG+AVMTGL AV +MK LM E	240
Query 241	YAAGKGLKLKVNAHGHLTYHNVQPIAALPEMHELNIGHAIIGQAVMTGLAAAVTDMKVLRE	240
Query 241	AR 242	
Sbjct 241	AR	
Sbjct 241	AR 242	

>pdb|3F4N|A **S** Chain A, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|B **S** Chain B, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|C **S** Chain C, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|D **S** Chain D, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|E **S** Chain E, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|F **S** Chain F, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|G **S** Chain G, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|H S Chain H, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis
Length=246

Score = 391 bits (1005), Expect = 3e-107, Method: Compositional matrix adjust.
Identities = 197/242 (81%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 4	MA+LLLGVNIDHIATLRNARGT YPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	
Query 61	LRQTLDRMNLEMAVTEEMLAIAAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Sbjct 64	LRQT+ TRMNLEMAVT+EM+ IA + KPHFCCLVPEKRQEVTEGGLDVAGQ DKM A	
Query 121	LRQTIQTRMNLEMAVTDEMDIACDIKPHFCCLVPEKRQEVTEGGLDVAGQVDKMTLAV	123
Sbjct 124	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
	RLAD GI VSLFIDAD QI AA GAP+IEIHTG YADA T E+ EL RIAKAAT	
Query 181	GRLADVGILVSLFIDADFRQIDAAVAAGAPYIEIHTGAYADASTVLERQAEMLRIKAAT	183
Sbjct 184	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
	+AA GLKVNAHGHLTYHNV+ IAA+PEMHELNIGHAIIG+AVMTGL AV +MK LM E	
Query 241	YAAGKGLKVNAHGHLTYHNVQPIAALPEMHELNIGHAIIGQAVMTGLAAAVTDMKVLRE	243
Sbjct 244	AR 242	
	AR	
Sbjct 244	AR 245	

>**ref|ZP_00833834.1| COG0854: Pyridoxal phosphate biosynthesis protein [Yersinia ATCC 29909]**
Length=243

Score = 390 bits (1003), Expect = 4e-107, Method: Compositional matrix adjust.
Identities = 195/242 (80%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MA+LLLGVNIDHIATLRNARGT YPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	
Query 61	LRQTLDRMNLEMAVTEEMLAIAAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LRQT+ TRMNLEMAVT+EM+ IA E +PHFCCLVPEKRQEVTEGGLDVAGQ DKM A	
Query 121	LRQTIQTRMNLEMAVTDEMDIACELQPHFCCLVPEKRQEVTEGGLDVAGQLDKMTIAV	120
Sbjct 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
	RL++AGI VSLFIDAD QI AA VGAP+IEIHTG YADA TD + EL RI KAAT	
Query 181	SRLSEAGILVSLFIDADPMRQIDAAVAVGAPYIEIHTGAYADATTDLVRQAEVLVITKAAT	180
Sbjct 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
	+AA GLKVNAHGHLTYHNV+ IAA+PEMHELNIGHAIIG+AVMTGL AV +MK LM E	
Query 241	YAAGKGLKVNAHGHLTYHNVQPIAALPEMHELNIGHAIIGQAVMTGLAAAVTDMKVLRE	240
Sbjct 241	AR 242	
	AR	
Sbjct 241	AR 242	

>**ref|ZP_00827187.1| COG0854: Pyridoxal phosphate biosynthesis protein [Yersinia ATCC 43969]**
Length=243

Score = 390 bits (1003), Expect = 4e-107, Method: Compositional matrix adjust.
Identities = 195/242 (80%), Positives = 210/242 (86%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MA+LLLGVNIDHIATLRNARGT YPDP+QAAFIAEQAGADGITVHLREDRRHITDRDVRI	
Query 61	LRQTLDRMNLEMAVTEEMLAIAAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LRQT+ TRMNLEMAVT+EM+ IA E +PHFCCLVPEKRQEVTEGGLDVAGQ DKM A	
Query 121	LRQTIQTRMNLEMAVTDEMDIACELQPHFCCLVPEKRQEVTEGGLDVAGQIDKMTIAV	120
Sbjct 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
	RLA+AGI VSLFIDAD QI AA VGAP+IEIHTG YADA TD + EL RI KAAT	
Query 181	SRLAEAGILVSLFIDADMRQIDAATVVGAPYIEIHTGAYADAITDLARQAEVLVITKAAT	180
Sbjct 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
	+AAS GLKVNAHGHLTYHNV+ IAA+PE+ ELNIGHAIIG+AVMTGL AV +MK LM E	
Query 241	YAASKGLKVNAHGHLTYHNVQPIAALPEIQLNEIGHAIIGQAVMTGLAAAVGDMKVLRE	240
Sbjct 241		

Query 241 AR 242
 Sbjct 241 AR 242

>**ref|YP_071394.1|** G pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseudotuberculosis IP 32953]
ref|YP_001873412.1| G pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseudotuberculosis IP 32953]
sp|Q3V7P0.1|PDXJ_YERPS RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
emb|CAH22125.1| G pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseudotuberculosis IP 32953]
gb|ACC89955.1| G pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseudotuberculosis IP 32953]
Length=243

GENE ID: 2956225 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseudotuberculosis IP 32953] (10 or fewer PubMed links)

Score = 390 bits (1003), Expect = 4e-107, Method: Compositional matrix adjust.
 Identities = 196/242 (80%), Positives = 208/242 (85%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MA+LLGVNIDHIATLRNARGT YPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTLDTRMNLEMAVTTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDACP	120
Sbjct 61	LRQT+ TRMNLEMAVT+EM+ IA + KPHFCCLVPEKRQEVTEGGLDVAGQ DKM	120
Query 121	KRLADAGIQVSLFIDADEEQIKAQAAEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	RLAD GI VSLFIDAD QI AA GAP+IEIHTG YADA T E+ EL RIAKAAT	180
Query 181	FAASGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+AA GLKVNA GHGLTYHNV+ IAA+PEMHELNIGHAIIG+AVMTGL AV +MK LM E	240
Query 241	YAAGKGLKVNAGHGLTYHNVQPIAALPEMHELNIGHAIIGQAVMTGLATAVTDMKVLRE	240
Sbjct 241	AR 242	

>**ref|YP_051364.1|** G pyridoxal phosphate biosynthetic protein PdxJ [Pectobacterium atrosepticum SCRI1043]
sp|Q3V7N3.1|PDXJ_ERWCT RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
emb|CAG76173.1| G pyridoxal phosphate biosynthetic protein [Pectobacterium atrosepticum SCRI1043]
Length=243

GENE ID: 2882129 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Pectobacterium atrosepticum SCRI1043] (10 or fewer PubMed links)

Score = 390 bits (1001), Expect = 7e-107, Method: Compositional matrix adjust.
 Identities = 194/242 (80%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIATLRNARGT YPDPVQAAF+AEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTLDTRMNLEMAVTTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDACP	120
Sbjct 61	LR+TL TRMNLEMAVTTEEML IA E KPHFCCLVPEKRQEVTEGGLDVAGQ++K+ +A	120
Query 121	KRLADAGIQVSLFIDADEEQIKAQAAEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	RL+ A I VSLFIDAD+ QI AA GA +IEIHTG YADA D + E RI AAT	180
Query 181	FAASGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+AA+ GLKVNA GHGLTYHNV IAA+PEMHELNIGHAIIGRAV++GLKDAVAEMK LM E	240
Query 241	YAAAGKGLKVNAGHGLTYHNVLPPIAALPEMHELNIGHAIIGRAVISGLKDAVAEMKSLMRE	240
Sbjct 241	AR 242	

>ref|YP_001479890.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Serratia p 568]

gb|ABV42762.1| G pyridoxal phosphate biosynthetic protein PdxJ [Serratia protea 568]
Length=243

GENE ID: 5606405 Spro_3666 | pyridoxal phosphate biosynthetic protein PdxJ [Serratia proteamaculans 568]

Score = 382 bits (981), Expect = 1e-104, Method: Compositional matrix adjust.
Identities = 192/242 (79%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

Query 1	MAELLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MA+LLLGVNIDHIATLRNARGT YPD PVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LRQT+ TRMNLEMAVT+EML IA+E KPHFCCLVPEKR+EVTTEGGLDVAGQ+DKM A	120
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	++LA AGI VSLFID D QI AA VGAP+IEIHTG YA+A+ + EL RIA AAT	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+AA GLKVNAHGHLTYHNV+ IAA+PEMHELNIGHAIIG+AVM GL AV +MK LM E	240
Query 241	YAAEKGKVNAGHHLTYHNVQPIAALPEMHELNIGHAIIGQAVMCGLPAAVTDMKLLMRE	240
Sbjct 241	AR 242	
Sbjct 241	AR 242	

>ref|YP_455464.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Sodalis gloss str. 'morsitans']

dbj|BAE75059.1| G pyridoxal phosphate biosynthetic protein [Sodalis glossinidius str. 'morsitans']
Length=243

GENE ID: 3866528 SG1784 | pyridoxal phosphate biosynthetic protein PdxJ [Sodalis glossinidius str. 'morsitans'] (10 or fewer PubMed links)

Score = 381 bits (978), Expect = 3e-104, Method: Compositional matrix adjust.
Identities = 187/242 (77%), Positives = 208/242 (85%), Gaps = 0/242 (0%)

Query 1	MAELLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ELLGVNIDHIATLRNARG A+PDPVQAAFIAEQAGADGITVHLREDRRHITDRDV++	60
Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LR+T+ TRMNLEMAVT+EML IA+ PHFCCLVPEKRQEVTEGGLDVAGQ DK+R A	120
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	L+ AGIQVSLFIDADE QI AAA+VGAP+IEIHTG YADA + +A E ARI + A	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	FA GLKVNAHGHL YHNVK +AA+ +M ELNIGHAI RAV+ GL DAV +MKRLM E	240
Query 241	FAVKLGLKVNAHGHLTYHNVKPVAALAQMELNIGHAIISRAVIGGLADAVRDMKRLMRE	240
Sbjct 241	AR 242	
Sbjct 241	AR 242	

>ref|NP_930557.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Photorhabdus subsp. laumondii TTO1]

sp|Q7N1X8.1| PDXJ PHOLL RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN

emb|CAE15711.1| G Pyridoxal phosphate biosynthetic protein PdxJ (PNP synthase) [Photorhabdus luminescens subsp. laumondii TTO1]
Length=243

GENE ID: 2803349 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Photorhabdus luminescens subsp. laumondii TTO1] (10 or fewer PubMed links)

Score = 376 bits (966), Expect = 7e-103, Method: Compositional matrix adjust.
Identities = 184/242 (76%), Positives = 208/242 (85%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAE+LLGVNIDHIAT+RNARGT YPDPVQAAF+AEQAGADGIT+HLREDRRHITDRDV +	
Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDACP L++T+ TRMNLEMAVT+EM+ IA KP FCCLVPEKRQEVTTEGGLDV GQ+DK+ A	120
Sbjct 61	LKKTIQTRMNLEMAVTDEMV DIACRIKPEFCCLVPEKRQEVTTEGGLDVIGQKDKVAAAV	120
Query 121	KRLADAGIQVSLFIDA DEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARI AKAAT	180
Sbjct 121	KRL+DAGI VSLFIDA+ QI AA EVGAPFIEIHTG YADAK + EQ + E RI AAT	180
Query 181	FAASLGLKVNA GHGLTYHNVKAIAAIP EMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AAS GL VNAGHGLTYHNV+ IAA+PE++ELNIGHAIIGRAV +GL AVA+MK M +	240
Sbjct 181	YAASKGLTVNA GHGLTYHNVQRIAALPEIYELNIGHAIIGRAVFSGLTAAVADMKTQMRK	240
Query 241	AR 242	
Sbjct 241	AR 242	

>**ref|YP_855346.1| G pyridoxal phosphate biosynthetic protein PdxJ [Aeromonas hyd subsp. hydrophila ATCC 7966]**

gb|ABK38566.1| G pyridoxal phosphate biosynthetic protein PdxJ [Aeromonas hydro subsp. hydrophila ATCC 7966]
Length=245

GENE ID: 4487304 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Aeromonas hydrophila subsp. hydrophila ATCC 7966] (10 or fewer PubMed links)

Score = 376 bits (965), Expect = 9e-103, Method: Compositional matrix adjust.
Identities = 187/242 (77%), Positives = 203/242 (83%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MSEIYLGVNIDHIATLRNARGTQYPDPVQAAFVAEQAGADGITVHLREDRRHITDRDVEI	60
Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDACP LRQT+ TRMNLEMAVT+EM+ IA +PHF CLVPEKR EVTTEGGLDVAGQ DK+ DA	120
Sbjct 61	LRQTIQTRMNLEMAVTEEMI GIA CRI QPHFVCLVPEKR TEVTTEGGLDVAGQLDKVTD A V	120
Query 121	KRLADAGIQVSLFIDA DEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARI AKAAT	180
Sbjct 121	RL+ G QVSLFIDAD QI AAAE GAPFIEIHTG YADA TDAE+ E RIA A+ ARLSAVGAQVSLFIDA DPLQIDAAAESGAPFIEIHTGRYADATTDAERNAEFKRIAAGAS	180
Query 181	FAASLGLKVNA GHGLTYHNVKAIAAIP EMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AA GLKVNA GHGL YHNVKAIAAIP+E+ELNIGHAIIGRA GL AV++M+ LM E	240
Sbjct 181	YAAGKGLKVNA GHGLHYHNVKAIAAIP ELYELNIGHAIIGRAAFDGLAKAVSDMRLMQE	240
Query 241	AR 242	
Sbjct 241	AR 242	

>**ref|ZP_03318787.1| hypothetical protein PROVALCAL_01725 [Providencia alcalifaci DSM 30120]**

gb|EEB46268.1| hypothetical protein PROVALCAL_01725 [Providencia alcalifaciens DSM 30120]
Length=243

Score = 373 bits (958), Expect = 7e-102, Method: Compositional matrix adjust.
Identities = 180/242 (74%), Positives = 206/242 (85%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIAT+RNARGT YPDPVQAAF+AEQAGADGIT+HLREDRRHITDRDV +	
Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDACP L +T+ TRMNLEMAVT+EM+ IA KP +CCLVPEKR+EVTTEGGLDVAGQ+ K+ A	120
Sbjct 61	LNKTIQTRMNLEMAVTEEMI DIA CRI KPTYCC LVPEK REEV TTEGGLDVAGQKQKVAF A V	120
Query 121	KRLADAGIQVSLFIDA DEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARI AKAAT	180

Sbjct	121	KRL DAGI VSLFIDAD +QI AA E GAPFIEIHTG YADAKT+ EQ E RI + KRLTDAGILVSLFIDADHKQIDAAQECGAPFIEIHTGAYADAKTEQEQELEFRRIRDGV	180
Query	181	FAASLGLKVNAHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AA G+KVNAGHGLTYHNV+ IAA+PE++ELNIGHAIIGRA+ +GL AV++MK L++E	240
Sbjct	181	YAAGKGIKVNAHGLTYHNVQRIAALPEIYELNIGHAIIGRALFSGLSQAVSDMKNLLIE	240
Query	241	AR 242	
Sbjct	241	AR 242	

>**ref|ZP_02961267.1|** hypothetical protein PROSTU_03281 [Providencia stuartii ATCC 25827]
gb|EDU60077.1| hypothetical protein PROSTU_03281 [Providencia stuartii ATCC 25827]
Length=243

Score = 373 bits (957), Expect = 7e-102, Method: Compositional matrix adjust.
Identities = 182/242 (75%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI MAELLLGVNIDHIAT+RNARGT YPDPVQAAF+AEQAGADGITVHLREDRRHITDRD+ +	60
Sbjct	1	MAELLLGVNIDHIATVRNARGTQYPDPVQAAFVAEQAGADGITVHLREDRRHITDRDIEL	60
Query	61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC L++T+ TRMNLEMAVTEEM+ IA KP FCCLVPEKR+EVTTEGGLDVAGQ K+ DA	120
Sbjct	61	LKETIQTRMNLEMAVTEEMINIACRVKPAFCCLVPEKREEVTEGGLDVAGQLPKITDAV	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT KRL +AGIQVSLFIDAD QI AA GAPFIEIHTG YADAKT+ EQ E RI	180
Sbjct	121	KRLTEAGIQVSLFIDADHTQIDAAQAGAPFIEIHTGAYADAKTEQEIEYRRIRDGVA	180
Query	181	FAASLGLKVNAHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AA GLKVNAGHGLTYHNV+ IA +PE++ELNIGHAIIGRA+ +GL +AVA+MK+L+ E	240
Sbjct	181	YAAGKGLKVNAHGLTYHNVQRIALLPEIYELNIGHAIIGRALFSGLANAVADMKKLLRE	240
Query	241	AR 242	
Sbjct	241	AR 242	

>**ref|YP_002151612.1|** **G** pyridoxal phosphate biosynthetic protein [Proteus mirabilis]
emb|CAR43908.1| **G** pyridoxal phosphate biosynthetic protein [Proteus mirabilis H]
Length=243

GENE ID: 6803577 pdxJ | pyridoxal phosphate biosynthetic protein
[Proteus mirabilis HI4320] (10 or fewer PubMed links)

Score = 372 bits (956), Expect = 1e-101, Method: Compositional matrix adjust.
Identities = 181/242 (74%), Positives = 206/242 (85%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI M+++LLGVNIDHIATLRNARGT YPDPVQAAFIAEQAGADGIT+HLREDRRHITDRD+ +	60
Sbjct	1	MSDILLGVNIDHIATLRNARGTYPDPVQAAFIAEQAGADGITIHLREDRRHITDRDML	60
Query	61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC + QT+ TR+NLEMAVTEEM+ IA +T+P FCCLVPEKRQEVTEGGLDV G +K+ DA	120
Sbjct	61	ISQTQVTRLNLEMAVTEEMIEIACQTQPDFCCLVPEKRQEVTEGGLDVGNEEKVADAI	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT KRL+ AGI+VSLFID D EQI AA VGAPFIEIHTG YADA+ + Q +E RI A T	180
Sbjct	121	KRLSLAGIKVSLFIDPDHEQINAADRVVGAPFIEIHTGAYADAEDEQAEKEFVRIRDAVT	180
Query	181	FAASLGLKVNAHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AAS GLKVNAGHGL YHNV+ IAA+PE++ELNIGHAIIGRAV +GL AV EMKRLM E	240
Sbjct	181	YAASKGLKVNAHGLHYHNVQRIAALPELYELNIGHAIIGRAVFSGLAPAVEEMKRLMRE	240
Query	241	AR 242	
Sbjct	241	AR 242	

>**ref|YP_001143199.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Aeromonas subsp. salmonicida A449]

gb|ABO91451.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Aeromonas salmonicida A449]

Length=245

Gene ID: 4996852 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
 [Aeromonas salmonicida subsp. salmonicida A449]

Score = 372 bits (954), Expect = 2e-101, Method: Compositional matrix adjust.
 Identities = 184/242 (76%), Positives = 201/242 (83%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ E+ LGVNIDHIATLRNARGT YPDPVQAAF+AEQAGADGITVHLREDRRHITDRDV I	60
Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDACP	120
Sbjct 61	LRQT+ TRMNLEMAVTEEM+ IA KPHF CLVPEKR EVTTEGGLDVAGO DK+ DA	120
Query 121	KRLADAGIQVSLFIDADEEQIKAIAAEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	RL+ G QVSLFIDAD QI AAA+ GAPFIEIHTG YADA TD ++ E RIA A+	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+AA GLKVNAHGHL YHNVKAIAAIPE++ELNIGHAIIGRA GL AV++M+ LM E	240
Query 241	YAAGKGLKVNAHGHLHYHNVKAIAAIPELYELNIGHAIIGRAFDGLTKAVSDMRLLMQE	240
Sbjct 241	AR 242 R VR 242	

>**ref|ZP_03315319.1| hypothetical protein PROVRUST_02121 [Providencia rustigianii DSM 454T]**
gb|EEB38919.1| hypothetical protein PROVRUST_02121 [Providencia rustigianii DSM 4541]
 Length=243

Score = 367 bits (942), Expect = 4e-100, Method: Compositional matrix adjust.
 Identities = 178/242 (73%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDHIAT+RNARGT YPDPVQAAF+AEQAGADGIT+HLREDRRHITDRDV +	60
Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDACP	120
Sbjct 61	L QT+ TRMNLEMAVT+EM+ IA KP +CCLVPEKR+EVTTEGGLDVAGO+ K+ A	120
Query 121	KRLADAGIQVSLFIDADEEQIKAIAAEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	KRL ++GI VSLFIDAD EOI AA E GAPFIEIHTG YADAKT+ Q E RI	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+AA G+KVNAHGHLTYHNV+ IAA+PE++ELNIGHAIIGRA+ +GL AV++MK+L+ E	240
Query 241	YAAGKGIKVNAHGHLTYHNVQRIAALPEIYELNIGHAIIGRALFSGLAQAVSDMKQLLTE	240
Sbjct 241	AR 242 AR AR 242	

>**ref|ZP_01262022.1| pyridoxal phosphate biosynthetic protein [Vibrio alginolytic 12G01]**
gb|EAS74655.1| pyridoxal phosphate biosynthetic protein [Vibrio alginolyticus 12G01]
 Length=244

Score = 361 bits (926), Expect = 3e-98, Method: Compositional matrix adjust.
 Identities = 174/242 (71%), Positives = 206/242 (85%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ + LGVNIDHIATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHITDRDVRI	60
Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDACP	120
Sbjct 61	LR+T+ TRMNLEMAVT+EM+ IA++TKP F CLVPEKR+E+TTEGGLDV GQ +K++ A	120
Query 121	KRLADAGIQVSLFIDADEEQIKAIAAEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	K+L DAGI+VSLFIDAD +QI+AA + GAPFIE+HTG YADA T+ EQ EL +IA A+	180
Sbjct 121	KKLTAGIKVSLFIDADQQIEAAKCGAPFIELHTGHYADATTEDEQQAELKKIAAGAS	180

Query	181	FAASLGLKVNAAGHGLTYHNVKAI AAI PEMHELNIGHAI I IGRAVMTGLKDAVAEMKRLMLE	240
		+A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+IIGRAV GL AVA+MK LM+E	
Sbjct	181	YAHDLGIIVNAGHGLTYHNVAPIAALPEIYELNIGHSIIGRAVFDGLNKAVADMKALMIE	240
Query	241	AR 242	
		AR	
Sbjct	241	AR 242	

>**ref|ZP_03385196.1|** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica serovar Typhi str. M223]
Length=192

Score = 360 bits (925), Expect = 4e-98, Method: Compositional matrix adjust.
Identities = 179/192 (93%), Positives = 183/192 (95%), Gaps = 0/192 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MAELLLGVNIDHIATLRNARGT YPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	
Query	61	LRQTL D TRMNLEMAVTEEMLAI A VETKPHFCCLVPEKRQEV T E G GLDVAGQRDKMRDAC	120
Sbjct	61	LRQTL TRMNLEMAVTEEMLAI A VET+PHFCCLVPEKRQEV T E G GLDVAGQRDKMRDAC	
Query	121	KRLADAGIQVSLFIDADEEQIKA AA EVGAPFIEIHTGCYADAKTDAEQAQELARI A KAAT	180
Sbjct	121	RLA AGIQVSLFIDADE QI AAAEVGAPFIEIHTGCY+A+A+TDAEQA+ELARIA AAT	
Query	181	FAASLGLKVNA G 192	
Sbjct	181	AA LGLKVNA G 192	
Query	181	LAARLGLKVNA G 192	

>**ref|YP_205467.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio fischeri ES114]

sp|Q5E317.1|PDXJ VIBF1 **G** RecName: Full=Pyridoxine 5'-phosphate synthase; Short=
gb|AAW86579.1| **G** pyridoxine 5'-phosphate synthase [Vibrio fischeri ES114]
Length=243

GENE ID: 3279332 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Vibrio fischeri ES114] (10 or fewer PubMed links)

Score = 360 bits (924), Expect = 5e-98, Method: Compositional matrix adjust.
Identities = 173/242 (71%), Positives = 210/242 (86%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	M+ +LLGVNIDH+ATLRNARGT YPDPV AA IAE+AGA GIT+HLREDRRHITDRDVRI	
Query	61	LRQTL D TRMNLEMAVTEEMLAI A VETKPHFCCLVPEKRQEV T E G GLDVAGQRDKMRDAC	120
Sbjct	61	LR+TL TRMNLEMAVT+EM+ IA+ETKP F CLVPEKR+E+TTEGGL+V+GQ +K++ A	
Query	121	KRLADAGIQVSLFIDADEEQIKA AA EVGAPFIEIHTGCYADAKTDAEQAQELARI A KAAT	180
Sbjct	121	++L +AGI+VSLFIDAD+EQI AA E GAPFIE+HTG YADA+T+ Q EL +IA A+	
Query	181	FAASLGLKVNA G 240	
Sbjct	181	+AAS GL VNAGHGLTYHNV+AIAA+PE++ELNIGH+I+GRA+ GL+ AVA+M R+ML	
Query	241	AR 242	
Sbjct	241	AR 242	

>**ref|YP_002073491.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio sp.]
gb|EDN55839.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio sp. Ex25]
Length=243

GENE ID: 6654483 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Vibrio sp. Ex25]

Score = 358 bits (920), Expect = 1e-97, Method: Compositional matrix adjust.
Identities = 173/242 (71%), Positives = 206/242 (85%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ + LGVNIDHIATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHIDRDVRI	60
Query 61	LROTLTTRMNLEMAVTEEMLAIAAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDACP LR+T+ TRMNLEMAVT+EM+ IA++T+P F CLVPEKR+E+TTEGGLDV GQ +K++ A	120
Sbjct 61	LRETIQTRMNLEMAVTDEMVEIALQTQPEFVCLVPEKREELTTEGGLDVVGQLEKKAAT	120
Query 121	KRLADAGIQVSLFIDADEEQIKAQAAEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT K+L DAGI+VSLFIDAD +QI+AA + GAPFIE+HTG YADA T+ EQ EL +IA A+	180
Sbjct 121	KKLTDAIGIKVSLFIDADRQQIEAAKKCGAPFIELHTGHYADATTEDEQQAELKKIAAGAS	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +A LG+ VNAGHHLTYHNV IAA+PE++ELNIGH+IIGRAV GL AVA+MK LM+E	240
Sbjct 181	YAHDLGIIVNAGHHLTYHNVAPIAALPEIYELNIGHSIIGRAVFDGLNKAVADMKALMIE	240
Query 241	AR 242	
Sbjct 241	AR 242	

>**ref|YP_002156883.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio fischeri MJ11]

gb|ACH66587.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio fischeri MJ11]
Length=243

Gene ID: 6806102 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Vibrio fischeri MJ11]

Score = 358 bits (919), Expect = 2e-97, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 210/242 (86%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MSSILLGVNIDHVATLRNARGTYPDPVHAAEIAERAGAAGITIHLREDRRHIDRDVRI	60
Query 61	LROTLTTRMNLEMAVTEEMLAIAAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDACP LR+TL TRMNLEMAVT+EM+ IA+ETKP F CLVPEKR+E+TTEGG+V+GQ +K++ A	120
Sbjct 61	LRETLQTRMNLEMAVTDEMVGIALETKPEFVCLVPEKREELTTEGGLNVGQLEKVKAAAT	120
Query 121	KRLADAGIQVSLFIDADEEQIKAQAAEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT ++L +AGI+VSLFIDAD++QI AA E GAPFIE+HTG YADA+T+ Q EL +IA A+	180
Sbjct 121	QKLTEAGIKVSLFIDADKKQIDAVERCGAPFIELHTGAYADAETEEAQQDELKKIAAGAS	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AAS GL VNAGHHLTYHNV+AIAA+PE++ELNIGH+I+GRA+ GL AV++M R+ML	240
Sbjct 181	YAASKGLIVNAGHHLTYHNVEAIAALPEIYELNIGHSIMGRAMFDGLEKAVSDMHRIMLG	240
Query 241	AR 242	
Sbjct 241	AR 242	

>**ref|ZP_03400922.1|** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica serovar Typhi str. AG3].
Length=191

Score = 357 bits (916), Expect = 5e-97, Method: Compositional matrix adjust.
Identities = 176/191 (92%), Positives = 183/191 (95%), Gaps = 0/191 (0%)

Query 53	ITDRDVRILRQTLTRMNLEMAVTEEMLAIAAVETKPHFCCLVPEKRQEVTEGGLDVAGQ +TDRDVRILRQTL TRMNLEMAVTEEMLAIAAVET+PHFCCLVPEKRQEVTEGGLDVAGQ	112
Sbjct 1	MTDRDVRILRQTLHTRMNLEMAVTEEMLAIAAVETRPHFCCLVPEKRQEVTEGGLDVAGQ	60
Query 113	RDKMRDACKRLADAGIQVSLFIDADEEQIKAQAAEVGAPFIEIHTGCYADAKTDAEQAQEL RDKMRDAC RLA AGIQVSLFIDADE QI AAAEVGAPFIEIHTGCY+A+TDAEQA+EL	172
Sbjct 61	RDKMRDACARLAAAGIQVSLFIDADERQINAQAAEVGAPFIEIHTGCYANAETDAEQAQEL	120
Query 173	ARIAKAATFAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVA ARIA AAT AA LGLKVNAHGHLTYHNVKAIAA+PEMHELNIGHAIIGRAVMTGLK+AVA	232
Sbjct 121	ARIASAATLAARLGLKVNAHGHLTYHNVKAIAALPEMHELNIGHAIIGRAVMTGLKEAVA	180
Query 233	EMKRLMLEARG 243	
Sbjct 181	EMKRLMLEARG 191	

>**ref|NP_760465.1|** G pyridoxal phosphate biosynthetic protein PdxJ [Vibrio vulnificus CMCP6]
ref|NP_935621.1| G pyridoxal phosphate biosynthetic protein PdxJ [Vibrio vulnificus YJ016]
sp|Q8DC73.1|PDXJ_VIBVU RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
sp|Q7MHP1.1|PDXJ_VIBVY G RecName: Full=Pyridoxine 5'-phosphate synthase; Short=gb|AAO09992.1|AE016802_35 G Pyridoxal phosphate biosynthesis protein [Vibrio vulnificus YBAC95592.1] G pyridoxal phosphate biosynthesis protein [Vibrio vulnificus Y Length=243

GENE ID: 1178481 VV1_1568 | pyridoxal phosphate biosynthetic protein PdxJ [Vibrio vulnificus CMCP6] (10 or fewer PubMed links)

Score = 356 bits (914), Expect = 9e-97, Method: Compositional matrix adjust.
 Identities = 172/242 (71%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ + LGVNIDH+ATLRNARGT YPDPV AA +AE+AGADGIT+HLREDRRHITDRDVRI	60
Query 61	LRQTLQTRMNLEMAVTTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDACP	120
Sbjct 61	LR+TL TRMNLEMAVT+EM+ IA++T+P + CLVPEKR+E+TTEGGLDVAG DK++ A LRETLQTRMNLEMAVTDEMIEIALKTQPEYVCLVPEKREELTTEGGLDVAGHLDKIKAAT	120
Query 121	KRLADAGIQVSLFIDADEEQIKAQAAEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	++L AGI+VSLFIDAD EQI AA GAPFIE+HTG YADA T+A+Q EL +IA A+ EKLTAAGIKVSLFIDADREQIDAACAGAPFIELHTGHYADAATEADQLDELKKIAAGAS	180
Query 181	FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+AA LG+ VNAGHGLTYHNV IAA+PE++ELNIGHAIIGRAV GL AVA+MK +M+ YAADLGITVNAGHGLTYHNVAPIAALPEIYELNIGHAIIGRAVFDGLHKAVADMKAIMVA	240
Query 241	AR 242	
Sbjct 241	AR	
	AR 242	

>**ref|YP_131204.1|** G pyridoxal phosphate biosynthetic protein PdxJ [Photobacterium profundum SS9]
sp|Q3V7I6.1|PDXJ_PHOPR RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
emb|CAG21402.1| G putative pyridoxal phosphate biosynthetic protein PdxJ [Photobacterium profundum SS9] Length=243

GENE ID: 3123572 PBPRA3086 | pyridoxal phosphate biosynthetic protein PdxJ [Photobacterium profundum SS9] (10 or fewer PubMed links)

Score = 355 bits (912), Expect = 1e-96, Method: Compositional matrix adjust.
 Identities = 172/242 (71%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ + LLGVNIDH+ATLRNARGT YPDPV AA +AE+AGADGITVHLREDRRHITDRDVRI	60
Query 61	LRQTLDTRMNLEMAVTTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDACP	120
Sbjct 61	L++T+ TRMNLEMAVT+EM++IA++TKP F CLVPEKR+E+TTEGGLDVAGO +K++ A LKETIQTRMNLEMAVTDEMVSIALDTKPEFVCLVPEKREELTTEGGLDVAGQLEKIKAAT	120
Query 121	KRLADAGIQVSLFIDADEEQIKAQAAEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	++L DAGI+VSLFIDAD QI A GAPF+E+HTG YADA+T+ Q EL +IA AAT QKLTDAKIVSLFIDADRAQIDATLACGAPFVELHTGHYADAETEEAQQAELEKIASAAT	180
Query 181	FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+A LG+KVNAAGHGLTYHNVK IAA+PE++ELNIGH+II RA GL AVA+MK ML+ YAHLGIKVNAAGHGLTYHNVKPIAALPELYELNIGHSIISRAAFDGLNKAVADMKVEMLD	240
Query 241	AR 242	
Sbjct 241	AR	
	AR 242	

>**ref|ZP_01816562.1|** pyridoxal phosphate biosynthetic protein PdxJ [Vibrionales b SWAT-3]
gb|EDK26047.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrionales bacte SWAT-3]

Length=245

Score = 354 bits (909), Expect = 3e-96, Method: Compositional matrix adjust.
 Identities = 171/243 (70%), Positives = 204/243 (83%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ +LLGVNIDHIATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHI DRDVRI	60
Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Sbjct 61	L +T+ TRMNLEMAVT+EM+ IA++TKP F CLVPEKR+E+TTEGGLDV GQ DK++ A LAETIQTRMNLEMAVTDEMVKIALDTKPEFVCLVPEKREELTTEGGLDVGQLDKIKAAT	120
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
Sbjct 121	++L+ +AGI+VSLFIDAD EQI AA GAPFIE+HTG YADAKT+ +Q EL +IA A+ QKLSEAGIKVSLFIDADREQIDAACAGAPFIELHTGHYADAKTEEDQQDELKKIAAGAS	180
Query 181	FAASLGLKVNAAGHGLTYHNVKIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+I+GRAV GL AVA+MK +M YADDLGITVNAGHGLTYHNVAPIAALPEIYELNIGHSIMGRAVFDGLNKAVADMKAVMET	240
Query 241	ARG 243	
Sbjct 241	AR	
	ARN 243	

>**ref|YP_001906938.1|** **G** Pyridoxal phosphate biosynthetic protein (PNP synthase) [tasmaniensis Et1/99]

emb|CAO96041.1| **G** Pyridoxal phosphate biosynthetic protein (PNP synthase) [Erwinia tasmaniensis Et1/99]
 Length=243

GENE ID: **6299767 pdxJ** | Pyridoxal phosphate biosynthetic protein (PNP synthase)
 [Erwinia tasmaniensis Et1/99]

Score = 354 bits (908), Expect = 4e-96, Method: Compositional matrix adjust.
 Identities = 186/243 (76%), Positives = 205/243 (84%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	MAELLLGVNIDH+AT+RNARGT YPDPVQAAF++EQAGADGITVHLREDRRHI DRDVRI	60
Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LRQT+ TRMNLEMAVT+EM+ IA E +PHFCCLVPEKR+EVTTEGGLDVAGQ DK+ A LRQTIQTRMNLEMAVTDEMVDIACEIQPHFCCLVPEKREELTTEGGLDVAGQLDKVTAAV	120
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
Sbjct 121	KRL DAG+ VSLFIDAD QI AA GAP+IEIHTG YA+A + ELARIA AAT KRLNDAGVLVSLFIDADRGQIDAAVAAGAPYIEIHTGAYAEAPEGLARDTELARIAAAAAT	180
Query 181	FAASLGLKVNAAGHGLTYHNVKIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+AA GLKVNAAGHGLTYHNV IAA+PEM ELNIGHAIIGRAV +GL AV EMK+L+ YAAGKGLKVNAAGHGLTYHNVLPPIAALPEMVELNIGHAIIGRAVFSGLAAAVQEMKQLLRA	240
Query 241	ARG 243	
Sbjct 241	ARG	
	ARN 243	

>**ref|ZP_01161526.1|** pyridoxal phosphate biosynthetic protein [Photobacterium sp. SKA34]

gb|EAR54737.1| pyridoxal phosphate biosynthetic protein [Photobacterium sp. SKA34]
 Length=243

Score = 353 bits (906), Expect = 7e-96, Method: Compositional matrix adjust.
 Identities = 168/243 (69%), Positives = 208/243 (85%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M +LLGVNIDHIATLRNARGT+YPDPV AA +AE+AGADGIT+HLREDRRHI DRDVRI	60
Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LR+T+ TRMNLEMAVT+EM+AIA++ KP + CLVPEKR+E+TTEGGLDV+GQ +K++ A LRETIQTRMNLEMAVTDEMVAIALDVKPEYVCLVPEKREELTTEGGLDVSGQLEKVKAAAT	120
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
Sbjct 121	++L AGI+VSLFIDAD QI AA GAPFIE+HTG YA+AKT+ Q EL ++A A+	180

Sbjct	121	EKLTAAGIKVSLFIDADRAQIDAHHACGAPFIELHTGQYAEAKTEEAQLDELKKVAAGAS	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +A +LG+KVNAGHGLTYHNVK IAA+PE++ELNIGH+I+GRA+ GL+ +VA+M+ LM E	240
Sbjct	181	YAHNLGIKVNAAGHGLTYHNVKLIAALPELYELNIGHSIMGRAMFDGLEKSVADMRLMQE	240
Query	241	ARG 243	
Sbjct	241	ARG 243	

>**ref|YP_002127690.1|** **G** pyridoxal phosphate biosynthetic protein [Alteromonas mac 'Deep ecotype']

gb|ACG67696.1| **G** pyridoxal phosphate biosynthetic protein [Alteromonas macleodi 'Deep ecotype']
Length=250

Gene ID: 6778911 MADE 03404 | pyridoxal phosphate biosynthetic protein [Alteromonas macleodii-'Deep ecotype'] (10 or fewer PubMed links)

Score = 353 bits (905), Expect = 1e-95, Method: Compositional matrix adjust.
Identities = 176/242 (72%), Positives = 202/242 (83%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	6	M+ +LLGVNIDHIATLRNARGT YPDPV AA IAE+AGADGITVHLREDRRHIDRDVRI	65
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTEGGLDVAGQRDKMRDACP	120
Sbjct	66	L QT++TR+NLEMAVT+EMLAIA E KP FCCLVPEKR+E+TTEGGLDVAG D ++ AC LAQTINTRLNLEMAVTDEMLAIAEEVKPVFCCLVPEKREELTTEGGLDVAGNVDNIKAAAC	125
Query	121	KRLADAGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct	126	R LA+A I VSLFIDAD+ QI AAA AP+IEIHTG YA+A ++ Q +ELAR+ + DRLANANILVSLFIDADKAQIDAAAACNAPYIEIHTGQYAEATSEEAQQEELARLVEGIE	185
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	186	+A SLGLKVNAGHGL YHNVK IAAIP++ ELNIGHAIIR A GL AVA+M++LMLE YADSLGLKVNAGHGLHYHNVKPIAAIPQLIELNIGHAIIRAAFGLHKAVADMRLKLMLE	245
Query	241	AR 242	
Sbjct	246	AR 247	

>**ref|ZP_01870295.1|** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio shilon AK1]

gb|EDL51107.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio shilonii AK1]
Length=244

Score = 352 bits (904), Expect = 1e-95, Method: Compositional matrix adjust.
Identities = 170/242 (70%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	M+ +LLG+NIDHIATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHIDRDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTEGGLDVAGQRDKMRDACP	120
Sbjct	61	LR+TL TRMNLEMAVT+EM+ IA++T+P F CLVPEKR+E+TTEGGLDV GQ +K++ A LRETLQTRMNLEMAVTDEMIDIALKTQPEFVCLVPEKREELTTEGGLDVKGQLEKIAAT	120
Query	121	KRLADAGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	++L+ AGI+VSLFIDAD EQI AA GAPFIE+HTG YADA+T+ +Q EL +IA A+ EKLSAAGIKVSLFIDADREQIDAAGAAGAPFIELHTGHYADAETEEDQQDELKKIAAGAS	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	+AA +G+ VNAGHGLTYHNV IAA+PE++ELNIGH+IIGRAV GL AVA+MK +M YAADIGITVNAGHGLTYHNVAPIAAALPEIYELNIGHSIIGRAVFDGLHKAVADMKAVMES	240
Query	241	AR 242	
Sbjct	241	AR 242	

>**ref|YP_588729.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Baumannia cic str. Hc (Homalodisca coagulata)]

gb|ABF13930.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Baumannia cicad

str. Hc (Homalodisca coagulata)]
Length=243

GENE ID: 4056676 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Baumannia cicadellinicola str. Hc (Homalodisca coagulata)]
(10 or fewer PubMed links)

Score = 352 bits (904), Expect = 1e-95, Method: Compositional matrix adjust.
Identities = 166/243 (68%), Positives = 201/243 (82%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ LLL VNIDHIATLRNARGT +PDPVQAAFIAE AGADGITVHLREDRRHI DRDV +	
Query 61	MSRLLLNVNIDHIATLRNARGTTWPDPEKQAAFIAEDAGADGITVHLREDRRHINDRDVTM	60
Sbjct 61	LRQTLDTRMNLEMAITDDMIAIACSVVRPDLCCLVPEKRQELTTEGGLDVAQQKKKISNAI	120
Query 121	LRQ+ TRMNLEMA+T++M+AIA +P CCLVPEKQ+TTEGGLDVA Q+ K+ +A	
Sbjct 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
	L++AGI VSLFIDAD++QI+AAAE+G+P+IEIHTGCY+A+ + E EL RI +AA	
	YLLSEAGIMVSLFIDADKQQIEAAAEIGSPYIEIHTGCYANARNNTECIAELERIRQAAD	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+A SLGLKVNAHGHLTYHNV+ IA + +HELNIGH+II RA+++GL A+ M L+	
	YATSLGLKVNAHGHLTYHNVQDIAMLSFIHELNIGHSIISRAIISGLNQAIINMINLLHN	240
Query 241	ARS 243	
Sbjct 241	AR	
	ARS 243	

>**ref|ZP_01220096.1| pyridoxal phosphate biosynthetic protein [Photobacterium pro3TCK]**
>**gb|EAS43446.1| pyridoxal phosphate biosynthetic protein [Photobacterium profund3TCK]**
Length=243

Score = 352 bits (902), Expect = 2e-95, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ LLGVNIDHIATLRNARGT YPDPV AA +AE+AGADGITVHLREDRRHI DRDVRI	
Query 61	MNNILLGVNIDHIATLRNARGTRYPPDVHAAEVAERAGADGITVHLREDRRHINDRDVRI	60
Sbjct 61	LRQTLDTRMNLEMAVTDEMVSIALDTKPEFVCLVPEKREELTTEGGLDVAGQLEKIAAT	120
Sbjct 61	L++T+ TRMNLEMAVT+EM++IA++TKP F CLVPEKR+E+TTEGGLDVAGO +K++ A	
Query 121	LKETIQTRMNLEMAVTDEMVSIALDTKPEFVCLVPEKREELTTEGGLDVAGQLEKIAAT	120
Sbjct 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	++L AGI+VSLFIDAD QI A GAPF+E+HTG YADA+T+ Q EL +IA AAT	
Sbjct 121	QKLTAAGIKVSLFIDADRAQIDATLACGAPFVELHTGHYADAETEEAQQAELDKIASAAT	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+A LG+KVNAGHHLTYHNVK IAA+PE++ELNIGH+IIGRA GL AVA+MK +L+	
Sbjct 181	YAHGLGIKVNAHGHLTYHNVKPIAALPELYELNIGHSIIGRAAFDGLNKAVADMKVEVLD	240
Query 241	AR 242	
Sbjct 241	AR	
	AR 242	

>**ref|YP_002263870.1| G pyridoxal phosphate biosynthetic protein PdxJ [Aliivibrio LFI1238]**

>**emb|CAQ80206.1| G pyridoxal phosphate biosynthetic protein PdxJ [Aliivibrio sal LFI1238]**
Length=243

GENE ID: 6988220 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Vibrio salmonicida LFI1238]

Score = 352 bits (902), Expect = 2e-95, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ +LLGVNIDH+ATLRNARGT YPDPV AA IAE+AGA GIT+HLREDRRHI DRDVRI	
Query 61	MSSILLGVNIDHVATLRNARGTKYPDPVHAAEIAERAGAAGITIHLREDRRHI KDRDVRI	60
	LRQTLDTRMNLEMAVTDEMVSIALDTKPEFVCLVPEKREELTTEGGLDVAGQLEKIAAT	120

Sbjct	61	LR+TL TRMNLEMAVT+EM+ IA+ET+P F CLVPEKR+E+TTEGGL+V GQ +K++ A LRETIQTRMNLEMAVTDEMVGIALETQPEFVCLVPEKREELTTEGGLNVVGQLEKVKAAT	120
Query	121	KRLADAGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT + L+ AGI+VSLFIDAD QI AA GAPFIE+HTG YADA+T+ + EL +IA AT	180
Sbjct	121	QTLSKAGIKVSLFIDADNAQIDAACVACGAPFIELHTGAYADAETEEAEQIELKKIAAGAT	180
Query	181	FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AAS GL VNAGHGLTYHNV+AIAA+PE++ELNIGH+I+GRAV GL+ AVA+M R+ML	240
Sbjct	181	YAASKGLIVNAAGHGLTYHNVKAIAAIPEIYELNIGHSIMGRAVFDGLEKAVADMHRIMLG	240
Query	241	AR 242	
Sbjct	241	AR 242	

>**ref|ZP_01236135.1|** pyridoxal phosphate biosynthetic protein [Vibrio angustum S1
gb|EAS63814.1| pyridoxal phosphate biosynthetic protein [Vibrio angustum S14]
Length=243

Score = 352 bits (902), Expect = 2e-95, Method: Compositional matrix adjust.
Identities = 168/243 (69%), Positives = 207/243 (85%), Gaps = 0/243 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAEQAGADGITVHLREDRRHITDRDVRI M +LLGVNIDHIATLRNARGT YPDV AA +AE+AGADGIT+HLREDRRHIDRDVRI	60
Sbjct	1	MNNILLGVNIDHIATLRNARGTRYPDPVHAAEVAERAGADGITIHLREDRRHINDRDVRI	60
Query	61	LRQTLDRMNLEMAVTTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRD AC LR+T+ TRMNLEMAVT+EM+AIA+ KP + CLVPEKR+E+TTEGGLDVAGQ +K++ A	120
Sbjct	61	LRETIQTRMNLEMAVTDEMVAILDVKPEYVCLVPEKREELTTEGGLDVAGQLEKVKAAT	120
Query	121	KRLADAGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT ++L AGI+VSLFIDAD QI AA GAPFIE+HTG YA+A T+ Q+ EL ++A A+	180
Sbjct	121	EKLTAAGIKVSLFIDADRAQIDAACVACGAPFIELHTGQYAEATTEEAEQSDLKKVAA GAS	180
Query	181	FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +A +LG+ KVNAAGHGLTYHNVK IAA+PE++ELNIGH+I+GRA+ GL+ VA+M+ LM E	240
Sbjct	181	YAHNLGIKVNAAGHGLTYHNVKPIAALPELYELNIGHSIMGRAMFDGLEKSVADMRLLMQE	240
Query	241	ARG 243	
Sbjct	241	ARG 243	

>**gb|EED26525.1|** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio parahaemol
16]
Length=243

Score = 351 bits (901), Expect = 2e-95, Method: Compositional matrix adjust.
Identities = 169/242 (69%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAEQAGADGITVHLREDRRHITDRDVRI M+ + LGVNIDHIATLRNARGT YPDV AA +AE+AGADGIT+HLREDRRHIDRDVRI	60
Sbjct	1	MSSIYLGVNIDHIATLRNARGTKYPDPVHAAEVAERAGADGITIHLREDRRHINDRDVRI	60
Query	61	LRQTLDRMNLEMAVTTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRD AC LR+T+ TRMNLEMAVT+EM+ IA+ T+P + CLVPEKR+E+TTEGGLDV GQ +K++ A	120
Sbjct	61	LRETIQTRMNLEMAVTDEMVEIALNTQPEYVCLVPEKREELTTEGGLDVVGQLEKVKAAT	120
Query	121	KRLADAGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT ++L++AGI+VSLFIDAD EQI AA GAPFIE+HTG YADA+T+ +Q EL +IA A+	180
Sbjct	121	QKLSEAGIKVSLFIDADREQIDAACVACGAPFIELHTGHYADAETEEDQQDELKKVAA GAS	180
Query	181	FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +AA LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+I+GRA GL AVA+MK M+	240
Sbjct	181	YAADL GITVNAGHGLTYHNVAAIAAIP EYELNIGHSIIGRAAFDGLHKAVADMKAQMVL	240
Query	241	AR 242	
Sbjct	241	AR 242	

>**ref|ZP_01988133.1|** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio harvey
HY01]

ref|YP_001446696.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio har
ATCC BAA-1116]
gb|EDL67174.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio harveyi
HY01]

gb|ABU72469.1| **G** hypothetical protein VIBHAR_03533 [Vibrio harveyi ATCC BAA-111
Length=243

Score = 350 bits (899), Expect = 4e-95, Method: Compositional matrix adjust.
Identities = 168/242 (69%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ + LGVNIDHIATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHI DRDVRI	
Query 61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDACP LR+T+ TRMNLEMAVT+EM+ IA++TKP F CLVPEKR+E+TTEGGLDV GQ +K++ A	120
Sbjct 61	LRETIQTRMNLEMAVTDEMVEIALQTKPEFVCLVPEKREELTTEGGLDVVGQLEKVKAAT	120
Query 121	KRLADAGIQVSLFIDAEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT ++L +AGI+VSLFIDAD +QI AA GAP+IE+HTG YADA T+ +Q EL +IA A+	180
Sbjct 121	QKLTEAGIKVSLFIDAQQDAAKACGAPYIELHTGHYADATTEEDQQDELKKIAAGAS	180
Query 181	FAASLGLKVNAGHGLTYHNVKIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+IIGRAV GL+ +VAEMK +M+	240
Sbjct 181	YADDLGIIIVNAGHGLTYHNVAPIAAALPEIYELNIGHSIIGRAVFDGLEKSVAEMKAIMVA	240
Query 241	AR 242	
Sbjct 241	AR 242	

>**ref|ZP_01215567.1|** pyridoxal phosphate biosynthetic protein [Psychromonas sp. C
gb|EAS39633.1| pyridoxal phosphate biosynthetic protein [Psychromonas sp. CNPT3
Length=246

Score = 350 bits (899), Expect = 5e-95, Method: Compositional matrix adjust.
Identities = 174/242 (71%), Positives = 197/242 (81%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M++LLGVNIDH+ATLRNARGT YP+P A IAE +GADGIT+HLREDRRHI DRDV I	
Query 61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDACP L QTL TRMNLEMA+T+EM+ IA++TKP F CLVPEKR E+TTEGGLDVAG DK R A	120
Sbjct 61	LAQTLQTRMNLEMAITDEMIDIAIKTKPAFVCLVPEKRAELTTEGGLDVAGALDKTRSAV	120
Query 121	KRLADAGIQVSLFIDAEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT +RL AGIQVSLFIDAD+ QI AA GAP+IE+HTG YADA D QA EL R+A AT	180
Sbjct 121	QRLTQAGIQVSLFIDAQQDAAKACGAPYIELHTGHYADATTEEDQQDELKKIAAGAS	180
Query 181	FAASLGLKVNAGHGLTYHNVKIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +A LGLKVNAGHGL YHNVKIAAA+PE+ ELNIGHAI RA++ GL AV EMKRLM+E	240
Sbjct 181	YAHGLGLKVNAGHGLNYHNVKIAAAALPEIYELNIGHAIARALVDGLSVAQEMKRLMIE	240
Query 241	AR 242	
Sbjct 241	R 242	
Query 241	GR 242	

>**ref|ZP_01064680.1|** pyridoxal phosphate biosynthetic protein [Vibrio sp. MED222]
ref|YP_002418187.1| **G** Pyridoxal phosphate biosynthetic protein pdxJ [Vibrio spl
LGP32]
gb|EAQ53969.1| pyridoxal phosphate biosynthetic protein [Vibrio sp. MED222]
emb|CAV19823.1| **G** Pyridoxal phosphate biosynthetic protein pdxJ [Vibrio splendi
LGP32]
Length=245

Score = 349 bits (895), Expect = 1e-94, Method: Compositional matrix adjust.
Identities = 169/242 (69%), Positives = 202/242 (83%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ +LLGVNIDHIATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHI DRDVRI	
Query 61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDACP L +T+ TRMNLEMAVT+EM+ IA++T P F CLVPEKR+E+TTEGGLDV GQ +K++ A	120
Sbjct 61	LAETIQTMRNLEMAVTDEMVGQIALDTNPEFVCLVPEKREELTTEGGLDVVGQLEKIAAT	120
Query 121	KRLADAGIQVSLFIDAEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT ++L+ AGI+VSLFIDAD EQI AA GAPFIE+HTG YADAKT+ +Q EL +IA A+	180
Sbjct 121	EKLSAAGIKVSLFIDAQQDAAKACGAPFIELHTGHYADAKTEEDQQDELKKIAAGAS	180

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Query  181  FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE  240
          +A  LG+ VNAGHGLTYHNV  IAA+PE++ELNIGH+I+GRAV  GL  AVA+MK +M
Sbjct  181  YADDLGITVNAGHGLTYHNVAPIAALPEIYELNIGHSIMGRAVFDGLNKAVADMKAVMET  240

Query  241  AR  242
          AR
Sbjct  241  AR  242

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>**gb|EAZ49556.1|** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae V51]
Length=243

Score = 348 bits (893), Expect = 2e-94, Method: Compositional matrix adjust.
Identities = 172/242 (71%), Positives = 206/242 (85%), Gaps = 0/242 (0%)

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Query  1      MAELLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI  60
          M+ + LGVNIDH+ATLRNARGT+YPDPV AA  IAE+AGADGIT+HLREDRRHITDRDVRI
Sbjct  1      MSSIYLGVNIDHVATLRNARGTSYPDPVHAAEIAERAGADGITIHLREDRRHITDRDVRI  60

Query  61     LRQTLDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDAC  120
          LR+TL TRMNLEMAVT+EM+ IA++T+P + CLVPEKR+E+TTEGGLDV GQ ++++ A
Sbjct  61     LRETIQTRMNLEMAVTDEMVEIALQTQPEYVCLVPEKREELTTEGGLDVLGQLERVKAAT  120

Query  121    KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT  180
          ++L AGI+VSLFIDAD EQI AA  GAPFIE+HTG Y+DAK+D +Q EL +IA AA
Sbjct  121    EKLTAAGIKVSLFIDADREQIDAACAKACGAPFIELHTGHYSDAKSDVDQQNELKKIAAAA  180

Query  181    FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE  240
          +A  LG+ VNAGHGLTYHNV  IAA+PE++ELNIGHAIIGRAV  GL  AVA+MK +M+
Sbjct  181    YAHDLGITVNAGHGLTYHNVAAIAAIPEIYELNIGHAIIGRAVFDGLAKAVADMKAIMVA  240

Query  241    AR  242
          AR
Sbjct  241    AR  242

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>**ref|NP_798948.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio paraha RIMD 2210633]
sp|Q87LP2.1|PDXJ_VIBPA RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
dbj|BAC60832.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio paraha RIMD 2210633]
Length=243

GENE ID: 1190093 VP2569 | pyridoxal phosphate biosynthetic protein PdxJ [Vibrio parahaemolyticus RIMD 2210633] (10 or fewer PubMed links)

Score = 348 bits (892), Expect = 3e-94, Method: Compositional matrix adjust.
Identities = 173/242 (71%), Positives = 207/242 (85%), Gaps = 0/242 (0%)

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Query  1      MAELLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI  60
          M+ + LGVNIDHIATLRNARGT YPDPV AA  IAE+AGADGIT+HLREDRRHITDRDVRI
Sbjct  1      MSSIYLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRHILDRDVRI  60

Query  61     LRQTLDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDAC  120
          LR+T+ TRMNLEMAVT+EM+ IA++TKP F CLVPEKR+E+TTEGGLDV GQ DK++ A
Sbjct  61     LRETIQTRMNLEMAVTEEMVEIALKTKEFVCLVPEKREELTTEGGLDVGQLDKVKAAT  120

Query  121    KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT  180
          ++L +AGI+VSLFIDAD +QI+AA + GAPFIE+HTG YADA+T+ EQ EL +IA A+
Sbjct  121    QKLTEAGIKVSLFIDADRQQIEAAKQCGAPFIELHTGHYADAETEEQQAELKKIAAGAS  180

Query  181    FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE  240
          +A  LG+ VNAGHGLTYHNV  IAA+PE++ELNIGH+IIGRAV  GL+ +VAEMK LM+
Sbjct  181    YADDLGIVVNAGHGLTYHNVAPIAALPEIYELNIGHSIIGRAVFDGLEKSVAEMKALMIA  240

Query  241    AR  242
          AR
Sbjct  241    AR  242

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>**ref|ZP_00991369.1|** pyridoxal phosphate biosynthetic protein [Vibrio splendidus
gb|EAP93636.1| pyridoxal phosphate biosynthetic protein [Vibrio splendidus 12B0
Length=245

Score = 347 bits (890), Expect = 4e-94, Method: Compositional matrix adjust.
Identities = 168/242 (69%), Positives = 202/242 (83%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ +LLGVNIDHIATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHITDRDVRI	60
Query 61	LRQTLTTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTEGGLDVAGQRDKMRDACP	120
Sbjct 61	L +T+ TRMNLEMAVT+EM+ IA++T P F CLVPEKR+E+TTEGGLDV GQ +K++ A LAETIQTRMNLEMAVTDEMVCIALDTNPEFVCLVPEKREELTTEGGLDVVGQLEKIAAT	120
Query 121	KRLADAGIQVSLFIDADEEQIKAQAAEVGAPFIEHTGCYADAKTDAEQAQELARIKAAT	180
Sbjct 121	++L+ AGI+VSLFIDA+ EQI AA GAPFIE+HTG YADAKT+ +Q EL +IA A+ EKLSAAGIKVSLFIDAEREQIDAAKACGAPFIELHTGHYADAKTEEDQQDELKKIAAGAS	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+I+GRAV GL AVA+MK +M YADDLGITVNAGHGLTYHNVAPIAALPEIYELNIGHSIMGRAVFDGLNKAVADMKAVMET	240
Query 241	AR 242	
Sbjct 241	AR 242	

>**ref|NP_232087.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholera O1 biovar eltor str. N16961]
ref|ZP_01678308.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholera 2740-80T]
ref|ZP_01953186.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholera MAK 757T]
15 more sequence titles
ref|ZP_01957675.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholera MZO-3]
ref|ZP_01979577.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholera MZO-2]
ref|ZP_01983536.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholera 623-39]
ref|YP_002066631.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cho M010]
ref|YP_002069749.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cho RC385]
ref|YP_002174421.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cho AM-19226]
sp|Q9KPB5.1|PDXJ_VIBCH RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
gb|AAF95600.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae O1 biovar El Tor str. N16961]
gb|EAX57295.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae 2740-80]
gb|EAY37632.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae MAK 757]
gb|EAY40114.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae MZO-3]
gb|EDL71773.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae 623-39]
gb|EDM53535.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae MZO-2]
gb|EDN11667.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae RC385]
gb|EDN14389.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae AM-19226]
Length=243

GENE ID: 2613000 VC2458 | pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae O1 biovar eltor str. N16961] (10 or fewer PubMed links)

Score = 347 bits (890), Expect = 5e-94, Method: Compositional matrix adjust.
Identities = 172/242 (71%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ + LGVNIDH+ATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHITDRDVRI	60
Query 61	LRQTLTTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTEGGLDVAGQRDKMRDACP	120
Sbjct 61	LR+TL TRMNLEMAVT+EM+ IA++T+P + CLVPEKR+E+TTEGGLDV GQ +++++ A LRETLQTRMNLEMAVTDEMVEIALQTQPEYVCLVPEKREELTTEGGLDVLGQLERVKAAT	120

Query	121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEHTGCYADAKTDAEQAQELARIKAAT ++L AGI+VSLFIDAD EQI AA GAPFIE+HTG Y+DAK+D +Q EL +IA AA	180
Sbjct	121	EKLTAAGIKVSLFIDADREQIDAACAGCAGAPFIELHTGHYSDAKSDVDQQNELKKIAAAAAA	180
Query	181	FAASLGLKVNAAGHGLTYHNVKAIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +A LG+ VNAGHGLTYHNV AIAAYPE++ELNIGHAIIGRAV GL AVA+MK +M+	240
Sbjct	181	YAHDLGITVNAGHGLTYHNVAAIAAAIPEIYELNIGHAIIGRAVFDGLAKAVADMKAIMVA	240
Query	241	AR 242	
Sbjct	241	AR 242	

>**ref|ZP_02196848.1|** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio campbelli AND4]
gb|EDP58079.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio campbellii AND4]
Length=243

Score = 347 bits (889), Expect = 6e-94, Method: Compositional matrix adjust.
Identities = 166/242 (68%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI M+ + LGVNIDHIATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHIDRDVRI	60
Sbjct	1	MSSIYLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLDREDRRHILDRDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKQRQEVTEGGLDVAGQRDKMRDAC LR+T+ TRMNLEMAVT+EM+ IA++T+P F CLVPEKR+E+TTEGGLDVAGO +K++ A	120
Sbjct	61	LRETIQTRMNLEMAVTDEMVEIALKTQPEFVCLVPEKREELTTEGGLDVAGQLEKVKAAT	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEHTGCYADAKTDAEQAQELARIKAAT +L +AGI+VSLFIDAD +QI AA GAP++E+HTG YADA T+ +Q EL +IA A+	180
Sbjct	121	HKLTEAGIKVSLFIDADREQIDAACAGCAGAPYVELHTGHYADATTEEDQQDELKKIAAGAS	180
Query	181	FAASLGLKVNAAGHGLTYHNVKAIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +A LG+ VNAGHGLTYHNV AIAAYPE++ELNIGHAIIGRAV GL +VA+MK +M+	240
Sbjct	181	YADDLGIIIVNAGHGLTYHNVAPIALPEIYELNIGHSIIGRAVFDGLEKSADMKAIMVA	240
Query	241	AR 242	
Sbjct	241	AR 242	

>**ref|ZP_01681976.1|** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae V52]
ref|YP_001217960.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae O395]
gb|EAX61205.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae V52]
gb|ABQ21999.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae O395]
Length=243

Score = 347 bits (889), Expect = 7e-94, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI M+ + LGVNIDH+ATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHITDRDVRI	60
Sbjct	1	MSSIYLGVNIDHVATLRNARGTQYPDPVHAAEIAERAGADGITIHLDREDRRHITDRDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKQRQEVTEGGLDVAGQRDKMRDAC LR+TL TRMNLEMAVT+EM+ IA++T+P + CLVPEKR+E+TTEGGLDVAGO +++++ A	120
Sbjct	61	LRETLQTRMNLEMAVTDEMVEIALQTQPEYVCLVPEKREELTTEGGLDVQLERVKAAT	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEHTGCYADAKTDAEQAQELARIKAAT ++L AGI+VSLFIDAD EQI AA GAPFIE+HTG Y+DAK+D +Q EL +IA AA	180
Sbjct	121	EKLTAAGIKVSLFIDADREQIDAACAGCAGAPFIELHTGHYSDAKSDVDQQNELKKIAAAAAA	180
Query	181	FAASLGLKVNAAGHGLTYHNVKAIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +A LG+ VNAGHGLTYHNV AIAAYPE++ELNIGHAIIGRAV GL AV++MK +M+	240
Sbjct	181	YAHDLGITVNAGHGLTYHNVAAIAAAIPEIYELNIGHAIIGRAVFDGLAKAVSDMKAIMVA	240
Query	241	AR 242	
Sbjct	241	AR 242	

>**ref|ZP_01949430.1|** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae

1587]

gb|EAY34143.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae
1587]
Length=243

Score = 345 bits (886), Expect = 1e-93, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ + LGVNIDH+ATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHITDRDVRI	
Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LR+TL TRMNLEMAVT+EM+ IA++T+P + CLVPEKR+E+TTEGGLDV GQ ++++ A	
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
Sbjct 121	EKLTAAGIKVSLFIDADREQIDAACACGAPFIELHTGHYSDAKSDVDQQNELKKIAAAA	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+A G+ VNAGHHLTYHNV AIAAIP+E+ELNIGHAIIGRAV GL AVA+MK +M+	
Query 241	YAHDFGITVNAGHHLTYHNVAAIAAIP+EYELNIGHAIIGRAVFDGLAKAVADMKAIMVA	240
Query 241	AR 242	
Sbjct 241	AR	
Sbjct 241	AR 242	

>**ref|YP_663265.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Pseudoalteromon atlantica T6c]

gb|ABG42211.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Pseudoalteromon atlantica T6c]
Length=245

GENE ID: 4175489 Pat1 3709 | pyridoxal phosphate biosynthetic protein PdxJ [Pseudoalteromonas atlantica T6c]

Score = 345 bits (885), Expect = 2e-93, Method: Compositional matrix adjust.
Identities = 169/243 (69%), Positives = 200/243 (82%), Gaps = 0/243 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ + LGVNIDH+ATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHITDRDVRI	
Query 61	LRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDAC	120
Sbjct 61	LRQT++TR+NLEMAVT+EM+ IA+ T+P FCCLVPEKR+E+TTEGGLDV G + K+ DAC	
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
Sbjct 121	KQLSDAGILVSLFIDADFAQIDAACACNAPYIEIHTGQYAEAKNEAEQEAELAKLVAGIE	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+A + GLKVNAHGHL YHNVK IAAI ++ ELNIGHAI RA GL AV++M+ LMLE	
Query 241	YADAKGLKVNAHGHLHYHNVKPIAAIKQIIELNIGHAI IARAADFGLDKAVSDMRSLMLE	240
Query 241	ARG 243	
Sbjct 241	AR	
Sbjct 241	ARS 243	

>**ref|ZP_03354955.1|** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica serovar Typhi str. E01-6750]
Length=184

Score = 343 bits (881), Expect = 6e-93, Method: Compositional matrix adjust.
Identities = 169/184 (91%), Positives = 176/184 (95%), Gaps = 0/184 (0%)

Query 60	ILRQTLDRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDA	119
Sbjct 1	+LRQTL TRMNLEMAVTEEMLAIAVET+PHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDA	
Query 120	CKRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAA	179
Sbjct 61	C RLA AGIQVSLFIDADE QI AAAEVGAPFIEIHTGCY+A+TDAEQA+ELARIA AA	
Query 180	CARLAAAGIQVSLFIDADERQINAEEVGAPFIEIHTGCYANAETDAEQAQELARIASAA	120
Query 180	TFAASLGLKVNAHGHLTYHNVKAIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLML	239

Sbjct	121	T AA LGLKVNAGHGLTYHNVKAI AA +PEMHELNIGHAIIGRAVMTGLK+AVAEMKRLML TLAARLGLKVAGHGLTYHNVKAI AL PEMHELNIGHAIIGRAVMTGLKEAVAE M KRLML	180
Query	240	EARG 243	
Sbjct	181	EARG 184	

>**ref|ZP_01898798.1|** pyridoxal phosphate biosynthetic protein [Moritella sp. PE36]
gb|EDM66702.1| pyridoxal phosphate biosynthetic protein [Moritella sp. PE36]
Length=245

Score = 343 bits (880), Expect = 7e-93, Method: Compositional matrix adjust.
Identities = 167/242 (69%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct	1	M ++ LGVNIDHIATLR ARGT YPD P V AA +AE GADGITVHLREDRRHIDRDVR+ 60
Query	61	LRQTL D TRMNLEMAVTEEMLAI A VETKPHFCCLVPEKROEV T EGGLDVAGQRDKMRD A C 120
Sbjct	61	L++T+ TRMNLEMAVT EML IA E KP F CLVPEKR+E+TTEGGLDV GQ+DK+ A 120
Query	121	KRLADAGIQVSLFIDA EE QI AAA EVGAPFIEIHTGCYADAKTDAEQAQELARI A KAAT 180
Sbjct	121	KRL+ +AGI VSLFIDAD+E Q I AA GAP+IE+HTG YADA+++ EQ EL +IA + 180
Query	181	FAASLGLKVAGHGLTYHNVKAI AA IP M HELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct	181	YAHNAGLKVAGHGLHYHNVQPIA AA IP I YELNIGHAI I ARA A F G LGKAVKDMQVIMQE 240
Query	241	AR 242
Sbjct	241	AR 242

>**ref|ZP_03347562.1|** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica serovar Typhi str. E00-7866]
Length=179

Score = 340 bits (872), Expect = 6e-92, Method: Compositional matrix adjust.
Identities = 168/179 (93%), Positives = 172/179 (96%), Gaps = 0/179 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct	1	MAELLLGVNIDHIATLRNARGT YPD P VQAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Query	61	LRQTL D TRMNLEMAVTEEMLAI A VETKPHFCCLVPEKROEV T EGGLDVAGQRDKMRD A C 120
Sbjct	61	LRQTL H TRMNLEMAVTEEMLAI A VETRPHFCCLVPEKROEV T EGGLDVAGQRDKMRD A C 120
Query	121	KRLADAGIQVSLFIDA EE QI AAA EVGAPFIEIHTGCYADAKTDAEQAQELARI A KA 179
Sbjct	121	RLA AGIQVSLFIDA DE QI AAAEVGAPFIEIHTGCY+A+TDAEQA+ELARIA AA 179

>**ref|ZP_01614216.1|** pyridoxal phosphate biosynthetic protein [Alteromonadales TW-7]
gb|EAW26571.1| pyridoxal phosphate biosynthetic protein [Alteromonadales bacter TW-7]
Length=243

Score = 339 bits (869), Expect = 1e-91, Method: Compositional matrix adjust.
Identities = 162/242 (66%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct	1	M ++LLGVN+DHIA TL R ARGT YPD P AA +AE AGADGIT+HLREDRRHIDRDV+ 60
Query	61	LRQTL D TRMNLEMAVTEEMLAI A VETKPHFCCLVPEKROEV T EGGLDVAGQRDKMRD A C 120
Sbjct	61	+ +T+ TRMNLE AVT+EM+AIA+E KP + CLVPEKR+E+TTEGGLDVAG +K++ A 120
Query	121	KRLADAGIQVSLFIDA EE QI AAA EVGAPFIEIHTGCYADAKTDAEQAQELARI A KAAT 180
Sbjct	121	KLT D AGIKVSLFIDA D TAQLDAAKACGAPYVEIHTGAYADATNDSDL S KELEH I RQGVQ 180
Query	181	FAASLGLKVAGHGLTYHNVKAI AA IP M HELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct	181	+AASLGL VNAGHGL YHN V K IAA+PE++ELNIGHAI I RA + GL AV +MKRLM+E 240
		YAASLGLIVNAGHGLNYHNVKPIAAMPEIYELNIGHAI I ARA A IDGLDKAVRDMKRLMIE 240

Query 241 AR 242
 AR
 Sbjct 241 AR 242

>**ref|ZP_01450587.1|** pyridoxal phosphate biosynthetic protein [alpha proteobacter HTCC2255]
ref|ZP_03561535.1| pyridoxine 5'-phosphate synthase [Glaciecola sp. HTCC2999]
 Length=254

Score = 338 bits (866), Expect = 3e-91, Method: Compositional matrix adjust.
 Identities = 168/240 (70%), Positives = 196/240 (81%), Gaps = 0/240 (0%)

Query 3	ELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRILR	62
Sbjct 6	E+LLGVNIDH+ATLRNARGT+YPDPV AA IAE+AGADGITVHLREDRRHI DRDV IL EVLLGVNIDHVATLRNARGTSYPDPVHAADIAERAGADGITVHLREDRRHINDRDVEILA	65
Query 63	QTLDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGLDVAGQRDKMRDACKR +TL+TRMNLEMAVT+EMLAIA +T+P FCCLVPEKR E+TTEGGL+VAG +M+DAC +	122
Sbjct 66	RTLNTRMNLEMAVTDEMLAIAKKTQPAFCCLVPEKRAELTTEGGLNVAGNLSRMDACGQ	125
Query 123	LADAGIQVSLFIDAEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIKAATFA LA+ GI VSLFIDA+ EQI AA P+IEIHTG YADA + +Q QELA++ FA	182
Sbjct 126	LAEQGILVSLFIDAEPHQIDAACDVVPYIEIHTGQYADATSIIKQQTQELAKLKAGIQFA	185
Query 183	ASLGLKVNAGHGLTYHNVKIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLEAR GL+VNAGHGL YHNVK IAAIPE+ ELNIGHAI+ RA+ GL AV++M+ LM EAR	242
Sbjct 186	HQRGLQVNAGHGLHYHNVKPIAAIPEIVELNIGHAIMARAMFDGLGKAVSDMRALMQEAR	245

>**ref|YP_563765.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella denitribicans OS217]

gb|ABE56042.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella denitribicans OS217]
 Length=245

GENE ID: 4019282 Sden_2763 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella denitrificans OS217]

Score = 335 bits (860), Expect = 1e-90, Method: Compositional matrix adjust.
 Identities = 174/242 (71%), Positives = 197/242 (81%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVR M+ +LLG+NIDHIATLR ARGT YPDV AA +AE AGADGIT+HLREDRRHI DRDV +	60
Sbjct 1	MSGILLGINIDHIATLRQARGTNYPDPVHAAAEEHAGADGITIHLREDRRHIIDRDVYL	60
Query 61	LRQTLDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGLDVAGQRDKMRD L +TL TRMN E AVTEEM+AIA + KP + CLVPEKR+E+TTEGGLDVAGO DK+ A	120
Sbjct 61	LAALKTRMNFEFAVTEEMIAIACDVKPAYACLVPEKREELTTEGGLDVAGQMDKITA AAV	120
Query 121	KRLADAGIQVSLFIDAEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIKAAT RLA GI+VSLFIDAD QI AA GAP+IEIHTGCYADAK D+EQ A EL RI K A	180
Sbjct 121	SRLAAHGIKVSLFIDADATQIDAACVATGAPYIEIHTGCYADAKNDSEQAMELERITKMAK	180
Query 181	FAASLGLKVNAGHGLTYHNVKIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +A S GL VNAGHGL YHNVK IAAIPE++ELNIGHA+I RA + GL+ AV +MKRLMLE	240
Sbjct 181	YAHSKGLVVNAGHGLHYHNVKIAAAIPELYELNIGHAVIARAIDGLETAVRDMKRLMLE	240
Query 241	AR 242 R	
Sbjct 241	GR 242	

>**ref|YP_001553716.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella OS195]

gb|ABX48456.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella baltica OS195]
 Length=245

GENE ID: 5753009 Sbal195_1281 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella baltica OS195]

Score = 335 bits (859), Expect = 2e-90, Method: Compositional matrix adjust.
 Identities = 176/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVR 60

Sbjct 1	M+ +LLGVNIDHIATLR ARGT+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV + MSRILLGVNIDHIATLRQARGTSYYPDPVHAAVAEHAAGADGITIHLREDRRHIIDRDVYL	60
Query 61	LRQTLTTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTEGGLDVAGQ DK+ A	120
Sbjct 61	LAKTLKTRMNFECAVTEEMLNIACEIKPTVCLVPEKRQEVTEGGLDVAGQLDKITSAV	120
Query 121	KRLADAGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT RLA GIQVSLFIDAD+ QI AA GAP IEIHTGCYADAKT+AE+A ELARI++ A	180
Sbjct 121	TRLAAEGIQVSLFIDADKTQIDAASGAPLIEIHTGCYADAKTEAAEATELARISEMAK	180
Query 181	FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LM	240
Sbjct 181	YAHGKGLVVNAAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKVLML	240
Query 241	AR 242	
Sbjct 241	R GR 242	

>ref|YP_270774.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Colwellia psy 34H]
 sp|Q47WP8.1|PDXJ COLP3 **G** RecName: Full=Pyridoxine 5'-phosphate synthase; Short=
 gb|AAZ25393.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Colwellia psych 34H]
 Length=246

GENE ID: 3519304 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
 [Colwellia psychrerythraea 34H] (10 or fewer PubMed links)

Score = 335 bits (859), Expect = 2e-90, Method: Compositional matrix adjust.
 Identities = 167/242 (69%), Positives = 192/242 (79%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI M+ELLLGVN+DHIATLR ARGT YPDPV AA +AE AGADGITVHLREDRRHI DRD+ +	60
Sbjct 1	MSELLLGVNVDHIATLRQARGTNYPDPVYAAVASVAEHAAGADGITVHLREDRRHIQDRDIHV	60
Query 61	LRQTLTTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC L+QTL TRMN EMAVT+EM+AIA + KP FCCLVPEKR+E+TEGGLDV GQ DK+ A	120
Sbjct 61	LKQTLHTRMNFECAVTEEMLNIACEIKPTVCLVPEKRREELTTEGGLDVVGQLDKITKAT	120
Query 121	KRLADAGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT ++L AGI VSLFIDAD+ QI AA AP+IEIHTG YAD ++ EQ EL R+ Sbjct 121 EQLTAAGIAVSLFIDADKAQIDAASGAPLIEIHTGHYADLSSEEEQLIELERLTVGIK	180
Query 181	FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +A +LGLKVNAAGHGL Y NVK IAAI E+ ELNIGHAI RA + GL AV +MK+LM	240
Sbjct 181	YAHNLGLKVNAAGHGLNYFNVKPIAAIKEIIELNIGHAIVARAAIDGLDKAVRDMKQLMLE	240
Query 241	AR 242	
Sbjct 241	AR AR 242	

>ref|YP_734973.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp MR-4]
 gb|ABI39916.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. MR-4]
 Length=245

GENE ID: 4253416 Shewmr4_2845 | pyridoxal phosphate biosynthetic protein PdxJ
 [Shewanella sp. MR-4]

Score = 335 bits (858), Expect = 3e-90, Method: Compositional matrix adjust.
 Identities = 176/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI M+ +LLGVNIDHIATLR ARGT+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +	60
Sbjct 1	MSRILLGVNIDHIATLRQARGTSYYPDPVHAAVAEHAAGADGITIHLREDRRHIIDRDVYL	60
Query 61	LRQTLTTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTEGGLDVAGQ DK+ A	120
Sbjct 61	LAKTLKTRMNFECAVTEEMLNIACEVKPTVCLVPEKRQEVTEGGLDVAGQLDKITAAV	120
Query 121	KRLADAGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT RLA GIQVSLFIDAD+ QI AA E GAP IEIHTGCYADAKT E+A+ELARI++ A	180

Sbjct	121	SRLAANGIQVSLFIDADKTQIDAAVESGAPLIEHTGCYADAKTAEEEAKELARISEMAK	180
Query	181	FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE +A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE	240
Sbjct	181	YAHGKGLVVNAAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKALMLE	240
Query	241	AR 242	
Sbjct	241	R	
Sbjct	241	GR 242	

>**ref|YP_339261.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Pseudoalteromonas haloplanktis TAC125]

sp|Q3IDK9.1|PDXJ PSEHT G RecName: Full=Pyridoxine 5'-phosphate synthase; Short=
emb|CAI85818.1| **G** pyridoxine 5'-phosphate (PNP) synthase [Pseudoalteromonas haloplanktis TAC125]
Length=243

- **GENE ID: 3709965 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Pseudoalteromonas haloplanktis TAC125] (10 or fewer PubMed links)**

Score = 334 bits (856), Expect = 4e-90, Method: Compositional matrix adjust.
Identities = 161/242 (66%), Positives = 195/242 (80%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
		M ++LLGVN+DHIATLR ARGT+YPDP AA +AE AGADGIT+HLREDRRHIDRDV +	
Sbjct	1	MKDILLGVNVNDHIATLRQARGTSYPDPHAASVAEHAGADGITIHLREDRRHQDRDVYV	60
Query	61	LRQTLDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDAC	120
		+ +T+ TRMNLE AVT+EM+ IA+E KP + CLVPEKR+E+TTEGGLDVAG +K+ A	
Sbjct	61	MAKTIQTRMNLETAVTDEMINIALEVVKPEYVCLVPEKREELTTEGGLDVAGNLEKITAAT	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
		K L+DAGI+VSLFIDAD+ Q+ AA GAP++EIHTG YADA TD ++EL I +	
Sbjct	121	KTLSAGIKVSLFIDADKAQLDAAKATGAPYVEIHTGAYADATTDEAISKELEHIRQGVK	180
Query	181	FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+AAS+GL VNAGHGL YHNVK IAA+ E++ELNIGHAI RA + GL AV +MKRLMLE	
Sbjct	181	YAASIGLIVNAAGHGLHYHNVKPIAAAMEEYELNIGHAIVARAAIDGLDKAVRDMKRLMLE	240
Query	241	AR 242	
Sbjct	241	AR	
Sbjct	241	242	

>**ref|YP_002359017.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella OS223]

gb|ACK47594.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella baltica OS223]
Length=245

- **GENE ID: 7087887 Sbal223_3109 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella baltica OS223]**

Score = 334 bits (856), Expect = 4e-90, Method: Compositional matrix adjust.
Identities = 176/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
		M+ +LLGVNIDHIATLR ARGT+YPDPV AA +AE AGADGIT+HLREDRRHIDRDVY +	
Sbjct	1	MSRILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAQADGITIHLREDRRHIDRDVYL	60
Query	61	LRQTLDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDAC	120
		L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTEGGLDVAGQ DK+ A	
Sbjct	61	LAALKTRMNFECAVTEEMLNIACEIKPTVCLVPEKRQEVTTEGGLDVAGQLDKITAAV	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
		RLA GIQVSLFIDAD+ QI AA GAP IEIHTGCYADAKT+AE+A ELARI++ A	
Sbjct	121	TRLAAEGIQVSLFIDADKTQIDAAVAAGAPLIEIHTGCYADAKTEAEEATELARISEMAK	180
Query	181	FAASLGLKVNAAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE	
Sbjct	181	YAHGKGLVVNAAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKVLML	240
Query	241	AR 242	
Sbjct	241	R	
Sbjct	241	GR 242	

>ref|YP_001365462.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella OS185]

gb|ABS07399.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella balt OS185]
Length=245

GENE ID: 5372257 Shew185 1248 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella baltica OS185]

Score = 334 bits (856), Expect = 4e-90, Method: Compositional matrix adjust.
Identities = 176/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ +LLGVNIDHIATLR ARGT+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +	
Query 61	MSRILLGVNIDHIATLRQARGTSYPDPVHAAAEEAHAGADGITIHLREDRRHIDRDVYL	60
Sbjct 61	L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTEGGLDVAGO DK+ A	
Query 121	LRQTLDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRKQEVTEGGLDVAGQRDKMRDAC	120
Sbjct 121	LAKTLKTRMNFECAVTEEMLNIACEIKPTYVCLVPEKRQEVTTEGGLDVAGQLDKITAAV	120
Query 181	RLAEGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 181	RLA GIQVSLFIDAD+ QI AA GAP IEIHTGCYADAKT+AE+A ELARI++ A	
Query 241	FAASLGLKVNVAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 241	+A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE	
Query 241	YAHGKGLVVNVAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKVLML	240
Sbjct 241	AR 242	
	R	
Sbjct 241	GR 242	

>ref|YP_001182689.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella CN-32]

gb|ABP74890.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella putr CN-32]
Length=245

GENE ID: 5081572 Sputcn32 1162 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella putrefaciens CN-32]

Score = 333 bits (854), Expect = 8e-90, Method: Compositional matrix adjust.
Identities = 176/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ +LLGVNIDHIATLR ARGT+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +	
Query 61	MSRILLGVNIDHIATLRQARGTSYPDPVHAAAEEAHAGADGITIHLREDRRHIDRDVYL	60
Sbjct 61	L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTEGGLDVAGO DK+ A	
Query 121	LRQTLDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRKQEVTEGGLDVAGQRDKMRDAC	120
Sbjct 121	LAKTLKTRMNFECAVTEEMLNIACEIKPTYVCLVPEKRQEVTTEGGLDVAGQLDKITAAV	120
Query 181	RLAEGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 181	RLA GIQVSLFIDAD+ QI AA GAP IEIHTGCYADAKT+AE+A ELARI++ A	
Query 241	FAASLGLKVNVAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 241	+A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE	
Query 241	YAHGKGLVVNVAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKALMLE	240
Sbjct 241	AR 242	
	R	
Sbjct 241	GR 242	

>ref|YP_001049591.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella OS155]

gb|ABN60722.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella balt OS155]
Length=245

GENE ID: 4842456 Sbal 1204 | pyridoxal phosphate biosynthetic protein PdxJ

[Shewanella baltica OS155]

Score = 333 bits (853), Expect = 8e-90, Method: Compositional matrix adjust.
 Identities = 175/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ +LLGVNIDHIATLR ARGT+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +	
Query 61	MSRILLGVNIDHIATLRQARGTSYPPDVHAAAEEHAGADGITHLREDRRHIDRDVYL	60
Sbjct 61	LRQTLTTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
	L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTEGGLDVAGQ DK+ A	
	LAALKTRMNFECAVTEEMLNIACEIKPTVCLVPEKRQEVTEGGLDVAGQLDKITAAV	120
Query 121	KRLADAGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	RLA GIQVSLFIDAD+ QI AA GAP IEIHTGCYADAKT+A++A ELARI++ A	
Query 181	TRLAAEGIQVSLFIDADKTQIDAASGAPLIEIHTGCYADAKTEAQEATELARISEMAK	180
Sbjct 181	FAASLGLKVNAAGHGLTYHNVKIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
	+A GL VNAGHGL YHNVK AAAIPE++ELNIGHAI+ RA + GL AV +MK LM	
	YAHGKGLVVNAAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKVLMLE	240
Query 241	AR 242	
Sbjct 241	R	
	GR 242	

>**ref|YP_001500902.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella ATCC 700345]

gb|ABV86367.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella pealeana ATCC 700345]
 Length=245

GENE ID: 5661439 Spea_1040 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella pealeana ATCC 700345]

Score = 332 bits (852), Expect = 1e-89, Method: Compositional matrix adjust.
 Identities = 175/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ +LLGVNIDHIATLR ARGT+YPDPV AA +AE AGA+GIT+HLREDRRHI DRDV	
Query 61	MSRILLGVNIDHIATLRQARGTNYPDPVHAAAEEHAGAE GITIHLREDRRHIDRDVYT	60
Sbjct 61	LRQTLTTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
	L +TL TRMN EMAVTEEML IA E KP + CLVPEKR+E+TEGGLDVAGQ+DK+ A	
	LAALKTRMNFECAVTEEMLNIACEIKPAYVCLVPEKRELTTEGGLDVAGQQDKIAAV	120
Query 121	KRLADAGIQVSLFIDADEEQIKAEEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	RL GI+VSLFIDAD QI AA VGAP IEIHTGCYADA+TD+EQA EL RI + AT	
Query 181	ARLTKEGIKVSLFIDADSTQIDAASVGAPVIEIHTGCYADAETDSEQAAELKRITEMAT	180
Sbjct 181	FAASLGLKVNAAGHGLTYHNVKIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
	+A GL VNAGHGL YHNVKIAAAIPE++ELNIGHAI RA + GL AV +MK+LM	
	YAHGKGLVVNAAGHGLHYHNVKIAAAIPELYELNIGHAIARAAIDGLATAVRDMKQLMLE	240
Query 241	AR 242	
Sbjct 241	R	
	GR 242	

>**ref|YP_738968.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp MR-7]

gb|ABI43911.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. MR-7]
 Length=245

GENE ID: 4257702 Shewmr7_2927 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. MR-7]

Score = 332 bits (851), Expect = 2e-89, Method: Compositional matrix adjust.
 Identities = 175/242 (72%), Positives = 195/242 (80%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ +LLGVNIDHIATLR ARGT+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +	
Query 61	MSRILLGVNIDHIATLRQARGTSYPPDVHAAAEEHAGADGITHLREDRRHIDRDVYL	60
	LRQTLTTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
	L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTEGGLDVAGQ DK+ A	

Sbjct	61	LA KTLKTRMN FEC AVTE EMLN IA CEV KPT YVCL VPE KRQEV TTEG GLDV AGQL DKIT VAV	120
Query	121	KRLADAGI QVSLF IDA DEEQ QIK AAA EVG A P F IE HTGC YAD AKT DAE QAQ ELAR IAKA AT RLA GIQ VSLF IDAD + QI AA GAP IEI HTGC YAD AKT E+A +ELAR I++ A	180
Sbjct	121	SRLA ANGI QVSLF IDAD KTQI DAAV ASGA PLIE IHTGC YAD AKTA EEE AKEL ARI SEMA K	180
Query	181	FAASLGLK VNAGH GLTYH NVKA IAAI IPEM HELN IGHAI IGRA VMTGL KDAVA EMKRL MLE +A GL VNAGH GLYH NVKA IAAI IPE++ ELNIGH HAI+ RA + GL AV +MK LMLE	240
Sbjct	181	YAHGKGL VVNAGH GLHYH NVKPI AAIPE LYELN IGHAI VARAA IDGL ATAVK KDMK ALMLE	240
Query	241	AR R GR	242 242

>**ref|YP_751604.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella fr NCIMB 400]

gb|ABI72765.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella frig NCIMB 400]
Length=265

GENE ID: 4279831 Sfri 2926 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella frigidimarina NCIMB 400]

Score = 332 bits (851), Expect = 2e-89, Method: Compositional matrix adjust.
Identities = 173/239 (72%), Positives = 196/239 (82%), Gaps = 0/239 (0%)

Query	4	LLLGVN IDHI ATLR NARG TAYP DPVQ AAFI AEQAG ADGIT VHLRE DRRHT DRDV RILQ	63
Sbjct	24	+LLG+N IDHI ATLR ARGT YPD PV AA +AE AGAD GIT+ HLRE DRR HIDR D VYLL AK	83
Query	64	TLDTRM NLEM AVTE EMLA IAVET KPHFC CLVPE KRQEV TTEG GLDV AGQR DKMR DACK RL	123
Sbjct	84	TL TRMN E AVTE EM+A IA + KP + CLV PEKR+E +TTEG GLDV AGQ DK+R A RL TLK TRMN FEFA VTE EMIA ACDI KPAY ACLV PEK REEL TTEG GLDV AGQL DKIR SAV TRL	143
Query	124	ADAGI QVSLF IDA DEEQ QIK AAA EVG A P F IE HTGC YAD AKT DAE QAQ ELAR IAKA AT A GI+ VSLF IDAD + QI AA GAP +IEI HTGC YADA TDAE QA EL RI + A +A AAEGI KVSLF IDAD KTQI DAAV LSG S A P YIE HTGC YADA TDAE QA DEL VRITE MAQ YAH	183
Sbjct	144	AAEGIK VSLF IDAD KTQI DAAV LSG A P YIE HTGC YADA TDAE QA DEL VRITE MAQ YAH	203
Query	184	SLGLK VNAGH GLTYH NVKA IAAI IPEM HELN IGHAI IGRA VMTGL KDAVA EMKRL MLE S GL VNAGH GLYH NVKA IAAI IPE++ ELNIGH HAI+ RA + GL AV +MK+ LMLE R SKGL VVNAGH GLHYH NVKA IAAI IPELYEL NIGHAI VARAA IDGL ATAVK KDMK ALMLE	242
Sbjct	204	SKGL VVNAGH GLHYH NVKA IAAI IPELYEL NIGHAI VARAA IDGL ATAVK KDMK ALMLE	262

>**ref|YP_964373.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp W3-18-1]

ref|ZP_01706794.1| pyridoxal phosphate biosynthetic protein PdxJ [Shewanella pu 200]

gb|ABM25819.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. W3-18-1]

gb|EAY52920.1| pyridoxal phosphate biosynthetic protein PdxJ [Shewanella putref 200]
Length=245

GENE ID: 4661399 Sputw3181_3002 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. W3-18-1]

Score = 332 bits (850), Expect = 2e-89, Method: Compositional matrix adjust.
Identities = 175/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query	1	MAELL LGVN IDHI ATLR NARG TAYP DPVQ AAFI AEQAG ADGIT VHLRE DRRHT DRV I	60
Sbjct	1	M+ + LLGV NIDHI ATLR ARGT+ YPD PV AA +AE AGAD GIT+ HLRE DRR HIDR D VYLY	60
Query	61	LRTQL DTRM NLEM AVTE EMLA IAVET KPHFC CLVPE KRQEV TTEG GLDV AGQR DKMR DAC	120
Sbjct	61	L +TL TRMN E AVTE EM IA E KP + CLV PEKR QEV TTEG GLDV AGQ DK+ A LA KTL TRMN FEC AVTE EMLN IA CEV KPT YVCL VPE KRQEV TTEG GLDV AGQL DKIT AAV	120
Query	121	KRLADAGI QVSLF IDA DEEQ QIK AAA EVG A P F IE HTGC YAD AKT DAE QAQ ELAR IAKA AT RLA GIQ VSLF IDAD + QI AA GAP IEI HTGC YADA TDAE QA EL RI + A +A TRLAA EGI QVSLF IDAD KTQI DAAV ASGA PLIE IHTGC FADAK TEAEE AELAR RISE MAK	180
Sbjct	121	TRLAA EGI QVSLF IDAD KTQI DAAV ASGA PLIE IHTGC FADAK TEAEE AELAR RISE MAK	180
Query	181	FAASLGLK VNAGH GLTYH NVKA IAAI IPEM HELN IGHAI IGRA VMTGL KDAVA EMKRL MLE +A GL VNAGH GLYH NVKA IAAI IPE++ ELNIGH HAI+ RA + GL AV +MK LMLE	240
Sbjct	181	YAHGKGL VVNAGH GLHYH NVKA IAAI IPELYEL NIGHAI VARAA IDGL ATAVK KDMK ALMLE	240
Query	241	AR R GR	242

Sbjct 241 R GR 242

>ref|YP_001673314.1| G pyridoxal phosphate biosynthetic protein PdxJ [Shewanella HAW-EB4]

gb|ABZ75655.1| G pyridoxal phosphate biosynthetic protein PdxJ [Shewanella hali HAW-EB4]
Length=245

GENE ID: 5904608 Shal_1086 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella halifaxensis HAW-EB4]

Score = 330 bits (845), Expect = 7e-89, Method: Compositional matrix adjust.
Identities = 175/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M + LLGVNIDHIATLR ARGT YPDPV AA +AE AGA+GIT+HLREDRRHI DRDV	
Query 61	LRQTLDRMNLLEMMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDAC	120
Sbjct 61	L + TL TRMN EMAVTEEML IA + KP + CLVPEKR+E+TTEGGLDVAGQ+DK+ A	
Query 121	KRLADAGIQVSLFIDADEEQIKAIAEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
Sbjct 121	RL GI+VSLFIDAD+ QI AA VGAP IEIHTGCYADA+TDAEQA EL RI + AT	
Query 181	FAASLGLKVNVAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+A GL VNAGHGL YHNVKAIAAIPE++ELNIGHAI RA + GL AV +MK+LMLE	
Query 241	YAHGKGLVVNVAGHGLHYHNVKAIAAIPELYELNIGHAIIRAAIDGLATAVRDMKQLMLE	240
Sbjct 241	AR 242	
Sbjct 241	R GR 242	

>ref|YP_001093187.1| G pyridoxal phosphate biosynthetic protein PdxJ [Shewanella PV-4]

gb|ABO22928.1| G pyridoxal phosphate biosynthetic protein PdxJ [Shewanella loih PV-4]
Length=245

GENE ID: 4921109 Shew_1057 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella loihica PV-4]

Score = 329 bits (844), Expect = 1e-88, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 200/242 (82%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ + LGVNIDHIATLR ARGT+YPDPV AA +AE AGA+GITVHLREDRRHI DRD+ +	
Query 61	LRQTLDRMNLLEMMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDAC	120
Sbjct 61	L + T+ TRMN EMAVT+EML IA E KP + CLVPEKR+E+TTEGGLDVAGQ+DK+R A	
Query 121	KRLADAGIQVSLFIDADEEQIKAIAEVGAPFIEIHTGCYADAKTDAEQAQELARIKAAT	180
Sbjct 121	+RL GI+VSLFIDAD QI A VGAP IE+HTGCYADA+TDAEQA+ELARI + AT	
Query 181	FAASLGLKVNVAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+A GL VNAGHGL YHNVK+IAAIP+E++ELNIGHAI RA + GL AV +MK+LM+E	
Query 241	YAHGKGLVVNVAGHGLHYHNVKSIAAIPELYELNIGHAIIRAAIDGLDKAVRDMKQLMVE	240
Sbjct 241	AR 242	
Sbjct 241	R GR 242	

>ref|YP_001759633.1| G pyridoxal phosphate biosynthetic protein PdxJ [Shewanella ATCC 51908]

gb|ACA85538.1| G pyridoxal phosphate biosynthetic protein PdxJ [Shewanella wood ATCC 51908]
Length=245

GENE ID: 6115481 Swoo_1246 | pyridoxal phosphate biosynthetic protein PdxJ
[Shewanella woodyi ATCC 51908]

Score = 329 bits (844), Expect = 1e-88, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 197/242 (81%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ +LLGVNIDHIATLR ARGT+YPDPV AA +AE AGA+GITVHLREDRRHI DRD+ +	
Query 61	MSRILLGVNIDHIATLRQARGTSYPDPVHAAAEEHAGAEGITVHLREDRRHIVDRDIYL	60
Sbjct 61	LAKTLKTRMNFEAVTDEMLDIACEVKPAYVCLVPEKREELTTEGGLDVAGQMGKIESAV	120
Query 121	LRQTLTDMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Sbjct 121	L +TL TRMN EMAVT+EML IA E KP + CLVPEKR+E+TTEGGLDVAGO K+ A	
Query 181	LAKTLLKTRMNFEAVTDEMLDIACEVKPAYVCLVPEKREELTTEGGLDVAGQMGKIESAV	120
Sbjct 181	+RL D G++VSFLFIDAD+ QI AA VGAP IEIHTGCYADA DA+QA+ELARI + AT	
Query 241	QRLTDIGVKVSLFIDADKTQIDA AVAVGAPVIEIHTGCYADATNDADQAKELARITEMAT	180
Sbjct 241	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 241	+A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI RA + GL AV +MK+LM E	
Query 241	YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIARAAIDGLATAVKDMKQLMNE	240
Sbjct 241	AR 242	
Sbjct 241	R	
Sbjct 241	GR 242	

>**ref|YP_870654.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. ANA-3]

gb|ABK49248.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. ANA-3]
Length=245

GENE ID: 4478566 Shewana3_3023 | pyridoxal phosphate biosynthetic protein PdxJ
[Shewanella sp. ANA-3]

Score = 329 bits (843), Expect = 1e-88, Method: Compositional matrix adjust.
Identities = 174/242 (71%), Positives = 194/242 (80%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ +LLGVNIDHIATLR ARGT+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +	
Query 61	MSRILLGVNIDHIATLRQARGTSYPDPVHAAAEEHAGAEGITIHLREDRRHIDRDVYL	60
Sbjct 61	LAKTLLKTRMNFEAVTDEMLDIACEVKPAYVCLVPEKREELTTEGGLDVAGQQLDKITAAV	120
Query 121	LRQTLTDMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDAC	120
Sbjct 121	L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTEGGLDVAGO DK+ A	
Query 181	LAKTLLKTRMNFEAVTDEMLDIACEVKPAYVCLVPEKREELTTEGGLDVAGQQLDKITAAV	120
Sbjct 181	+RLA IQSLSFIDAD+ QI AA GAP IEIHTGCYADAKT E+A+ELARI++ A	
Query 241	SRLAANRIQSVLFIDADKTQIDA AVAAGAPLIEIHTGCYADAKTAEEEAKELARISEMAK	180
Sbjct 181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI RA + GL AV +MK LMLE	
Query 241	YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKALMLE	240
Sbjct 241	AR 242	
Sbjct 241	R	
Sbjct 241	GR 242	

>**ref|NP_716971.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella on MR-1]

sp|Q8EH78.1|PDXJ_SHEON RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
gb|AAN54416.1|AE015579_5 **G** pyridoxal phosphate biosynthetic protein PdxJ [Shew MR-1]
Length=245

GENE ID: 1169172 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Shewanella oneidensis MR-1] (10 or fewer PubMed links)

Score = 328 bits (842), Expect = 2e-88, Method: Compositional matrix adjust.
Identities = 174/242 (71%), Positives = 193/242 (79%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+ +LLGVNIDHIATLR ARGT+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +	
Query 61	MSRILLGVNIDHIATLRQARGTSYPDPVHAAAEEHAGAEGITIHLREDRRHIDRDVYL	60

Query 61	LRQTLDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRD	120
Sbjct 61	L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTEGGLDVAGQ DK+ A LA	120
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	RLA GIQVSLFIDAD+ QI AA GAP IEIHTGCYADAKT E+A+EL RI + A SRLAANGIQVSLFIDADKTQIDAASGAPLIEIHTGCYADAKTADDEAKELERIREMAK	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE YAHGKGLIVNAHGHLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKTLMLE	240
Query 241	AR 242	
Sbjct 241	R GR 242	

>**ref|YP_942095.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Psychromonas 37]

gb|ABM02496.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Psychromonas in 37]
Length=244

GENE ID: 4626841 Ping_0643 | pyridoxal phosphate biosynthetic protein PdxJ [Psychromonas ingrahamii 37]

Score = 328 bits (840), Expect = 3e-88, Method: Compositional matrix adjust.
Identities = 162/242 (66%), Positives = 192/242 (79%), Gaps = 0/242 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 1	M+++LLGVNIDHIATLRNARGT YP+P A IAE AGADGIT+HLREDRRH DRDV + MSQILLGVNIDHIATLRNARGTCYPEPAHLAAIAECAGADGITIHREDRRHINDRDVAV	60
Query 61	LRQTLDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRD	120
Sbjct 61	L QTL TRMNLEMAVT+EM+ IA++TKP F CLVPEKR+E+TTEGGL+V K+ A LAQTLQTRMNLEMAVTDEMVDIALKTPAFVCLVPEKREELTTEGGLNVVASFSKIASAV	120
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 121	RL A IQVSLFID + QI AA + GA +IE+HTG YADA ++ Q EL R+AKAAT SRLNAAAIQVSLFIDPENAQIDAAIKTGAAYIELHTGKYADAPSEDIQQFELMRVAKAAT	180
Query 181	FAASLGLKVNAHGHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct 181	+A+ G+KVNAHGHL YHNVK IAA+PE+ ELNIGHAI+ RA++ G AVAEMKRLM+E YASQAGIKVNAGHGLNYHNVKPIAAALPEIIELNIGHAIVARALVDGFGPAVAEMKRLMVE	240
Query 241	AR 242	
Sbjct 241	R GR 242	

>**ref|YP_693348.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Alcanivorax b SK2]

sp|Q0VP22.1|PDXJ ALCBS **G** RecName: Full=Pyridoxine 5'-phosphate synthase; Short=
emb|CAL17076.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Alcanivorax bo SK2]
Length=244

GENE ID: 4212451 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Alcanivorax borkumensis SK2] (10 or fewer PubMed links)

Score = 328 bits (840), Expect = 3e-88, Method: Compositional matrix adjust.
Identities = 163/238 (68%), Positives = 187/238 (78%), Gaps = 0/238 (0%)

Query 1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct 4	M+ +LLGVNIDHIATLR ARGT YP+PVQAA +AEQAGADGITVHLREDRRH DRDV + MSRVLLGVNIDHIATLRQARGTRYPEPVQAAALVAEQAGADGITVHLREDRRHINDRDVEL	63
Query 61	LRQTLDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRD	120
Sbjct 64	L QTL TRMNLEMA TEEM+ IA +P CCLVPEKR+E+TTEGGLDV G + + C LAQTLQTRMNLEMAATEEMVVIACRIQPPHCCLVPEKREELTTEGGLDVGNKAWIAQCC	123
Query 121	KRLADAGIQVSLFIDADEEQIKAAAEGAPFIEIHTGCYADAKTDAEQAQELARIAKAAT	180
Sbjct 124	+RL AGI+VSLFIDA+E QI AA E GAP IEIHTG YADA+T +Q QELARI A QRLGQAGIEVSLFIDAEEQSILAARECGAPAIEIHTGGYADAQTIDQQQQELARIIRSAVA	183

Query 181 FAASLGLKVNA
GHLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLM 238
FA + GL VNAGHGL YHN AIA IP ++ELNIGH+II RA +TGL +AV M+ L+
Sbjct 184 FALAQGLIVNA
GHGLHYHNTLAIAEIPGINELNIGHSIARAAITGLDEAVRSMRSLL 241

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